

# A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA LIBRARY. APPLICATION TO THE DETECTION OF MYCOBACTERIA

## I. Background of the invention

[001] The present invention pertains to a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC). The invention concerns also polynucleotides identified by the above method, as well as detection methods for mycobacteria, particularly *Mycobacterium tuberculosis*, and kits using said polynucleotides as primers or probes. Finally, the invention deals with BAC-based mycobacterium DNA libraries used in the method according to the invention and particularly BAC-based *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG DNA libraries.

[002] Radical measures are required to prevent the grim predictions of the World Health Organisation for the evolution of the global tuberculosis epidemic in the next century becoming a tragic reality. The powerful combination of genomics and bioinformatics is providing a wealth of information about the etiologic agent, *Mycobacterium tuberculosis*, that will facilitate the conception and development of new therapies. The start point for genome sequencing was the integrated map of the 4.4 Mb circular chromosome of the widely-used, virulent reference strain, *M. tuberculosis* H37Rv and appropriate cosmids were subjected to systematic shotgun sequence analysis at the Sanger Centre.

[003] Cosmid clones (Balasubramanian et al., 1996; Pavelka et al., 1996) have played a crucial role in the *M. tuberculosis* H37Rv genome sequencing project. However, problems such as under-representation of certain regions of the chromosome, unstable inserts and the relatively small insert size complicated the production of a comprehensive set of canonical cosmids representing the entire genome.

## II. Summary of the invention

[004] In order to avoid the numerous technical constraints encountered in the state of the art, as described hereabove, when using genomic mycobacterial DNA libraries constructed in cosmid clones, the inventors have attempted to realize genomic

mycobacterial DNA libraries in an alternative type of vectors, namely Bacterial Artificial Chromosome (BAC) vectors.

[005] The success of this approach depended on whether the resulting BAC clones could maintain large mycobacterial DNA inserts. There are various reports describing the successful construction of a BAC library for eucaryotic organisms (Cai et al., 1995; Kim et al., 1996; Misumi et al., 1997; Woo et al., 1994; Zimmer et al., 1997) where inserts up to 725 kb (Zimmer et al., 1997) were cloned and stably maintained in the *E. coli* host strain.

[006] Here, it is shown that, surprisingly, the BAC system can also be used for mycobacterial DNA, as 70% of the clones contained inserts in the size of 25 to 104 kb.

[007] This is the first time that bacterial, and specifically mycobacterial, DNA is cloned in such BAC vectors.

[008] In an attempt to obtain complete coverage of the genome with a minimal overlapping set of clones, a Bacterial Artificial Chromosome (BAC) library of *M. tuberculosis* was constructed, using the vector pBeloBAC11 (Kim et al., 1996) which combines a simple phenotypic screen for recombinant clones with the stable propagation of large inserts (Shizuya et al., 1992). The BAC cloning system is based on the *E. coli* F-factor, whose replication is strictly controlled and thus ensures stable maintenance of large constructs (Willems et al., 1987). BACs have been widely used for cloning of DNA from various eucaryotic species (Cai et al., 1995; Kim et al., 1996; Misumi et al., 1997; Woo et al., 1994; Zimmer et al., 1997). In contrast, to our knowledge this report describes the first attempt to use the BAC system for cloning bacterial DNA.

[009] A central advantage of the BAC cloning system over cosmid vectors used in prior art is that the F-plasmid is present in only one or a maximum of two copies per cell, reducing the potential for recombination between DNA fragments and, more importantly, avoiding the lethal overexpression of cloned bacterial genes. However, the presence of the BAC as just a single copy means that plasmid DNA has to be extracted from a large volume of culture to obtain sufficient DNA for sequencing and it is described here in the examples a simplified protocol to achieve this.

[010] Further, the stability and fidelity of maintenance of the clones in the BAC library represent ideal characteristics for the identification of genomic differences possibly responsible for phenotypic variations in different mycobacterial species.

[011] As it will be shown herein, BACs can be allied with conventional hybridization techniques for refined analyses of genomes and transcriptional activity from different mycobacterial species.

[012] Having established a reliable procedure to screen for genomic polymorphisms, it is now possible to conduct these comparisons on a more systematic basis than in prior art using representative BACs throughout the chromosome and genomic DNA from a variety of mycobacterial species.

[013] As another approach to display genomic polymorphisms, the inventors have also started to use selected H37Rv BACs for "molecular combing" experiments in combination with fluorescent *in situ* hybridization (Bensimon et al., 1994; Michalet et al., 1997). With such techniques the one skilled in the art is enabled to explore the genome of mycobacteria in general and of *M. tuberculosis* in particular for further polymorphic regions.

[014] The availability of BAC-based genomic mycobacterial DNA libraries constructed by the inventors have allowed them to design methods and means both useful to identify genomic regions of interest of pathogenic mycobacteria, such as *Mycobacterium tuberculosis*, that have no counterpart in the corresponding non-pathogenic strains, such as *Mycobacterium bovis* BCG, and useful to detect the presence of polynucleotides belonging to a specific mycobacterium strain in a biological sample.

[015] By a biological sample according to the present invention, it is notably intended a biological fluid, such as plasma, blood, urine or saliva, or a tissue, such as a biopsy.

[016] Thus, a first object of the invention consists of a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC).

[017] The invention is also directed to a polynucleotide of interest that has been isolated according to the above method and in particular a polynucleotide containing one or several Open Reading Frames (ORFs), for example ORFs encoding either a polypeptide involved in the pathogenicity of a mycobacterium strain or ORFs encoding Polymorphic Glycine Rich Sequences (PGRS).

[018] Such polynucleotides of interest may serve as probes or primers in order to detect the presence of a specific mycobacterium strain in a biological sample or to detect the expression of specific genes in a particular mycobacterial strain of interest.

[019] The BAC-based genomic mycobacterial DNA libraries generated by the present inventors are also part of the invention, as well as each of the recombinant BAC clones and the DNA insert contained in each of said recombinant BAC clones.

[020] The invention also pertains to methods and kits for detecting a specific mycobacterium in a biological sample using either at least one recombinant BAC clone or at least one polynucleotide according to the invention, as well as to methods and kits to detect the expression of one or several specific genes of a given mycobacterial strain present in a biological sample.

### **III. Brief description of the Figures.**

[021] In order to better understand the present invention, reference will be made to the appended figures which depicted specific embodiments to which the present invention is in no case limited in scope with.

[022] **Figures 1A and 1B** : PCR-screening for unique BAC clones with specific primers for 2 selected genomic regions of the H37Rv chromosome, using 21 pools representating 2016 BACs (Figure 1A) and sets of 20 subpools from selected positive pools (Figure 1B).

[023] **Figure 2** : Pulsed-field gel electrophoresis gel of *Dra*I- cleaved BAC clones used for estimating the insert sizes of BACs.

[024] **Figure 3** : Minimal overlapping BAC map of *M. tuberculosis* H37Rv superimposed on the integrated physical and genetic map established by Philipp et al. (18). Y- and I- numbers show pYUB328 (2) and pYUB412 (16) cosmids which were shotgun sequenced during the H37Rv genome sequencing project. Y-cosmids marked with \* were shown in the integrated physical and genetic map (18). Rv numbers show the position of representative BAC clones relative to sequenced Y- and I- clones. Squared Rv numbers show BACs which were shotgun sequenced at the Sanger Centre.

[025] **Figures 4A and 4B** : Ethidium bromide stained gel (Figure 4A) and corresponding Southern blot (Figure 4B) of *Eco*RI and *Pvu*II digested Rv58 DNA hybridized with <sup>32</sup>P labeled genomic DNA preparations from *M. tuberculosis* H37Rv, *M. bovis* ATCC 19210 and *M. bovis* BCG Pasteur.

[026] **Figure 5** : Organisation of the ORFs in the 12.7 kb genomic region present in *M. tuberculosis* H37Rv but not present in *M. bovis* ATCC 19210 and *M. bovis* BCG



Pasteur. Arrows show the direction of transcription of the putative genes. Positions of *EcoRI* and *PvuII* restriction sites are shown. Vertical dashes represent stop codons. The 11 ORFs correspond to the ORFs MTCY277.28 to MTCY277.38 / accession number Z79701 -EMBL Nucleotide Sequence Data Library. The junction sequences flanking the polymorphic region are shown.

[027] **Figure 6** : Variation in the C-terminal part of a PE-PGRS open reading frame in *M. tuberculosis* strain H37Rv relative to *M. bovis* BCG strain Pasteur.

[028] The numbers on the right side of the Figure denote the position of the end nucleotides, taking as the reference the *M. tuberculosis* genome.

[029] **Figure 7** : Polynucleotide sequence next to the *HindIII* cloning site in the BAC vector pBeloBAC11 (Kim et al., 1996) used to clone the inserts of the BAC-based mycobacterial genomic DNA library according to the invention.

[030] *NotI* : location of the *NotI* restriction sites.

[031] Primer T7-BAC1 : nucleotide region recognized by the T7-BAC1 primer shown in Table 1.

[032] T7 promoter: location of the T7 promoter region on the pBeloBac11 vector.

[033] Primer T7-Belo2 : nucleotide region recognized by the T7-Belo2 primer shown in Table 1.

[034] *Hind III* : the *HindIII* cloning site used to clone the genomic inserts in the pBeloBAC11 vector.

[035] SP6-Mid primer: nucleotide region recognized by the SP6 Mid primer shown in Table 1.

[036] SP6-BAC1 primer : nucleotide region recognized by the SP6 BAC1 primer shown in Table 1.

[037] SP6 promoter: location of the SP6 promoter region on the pBeloBac11 vector.

#### **IV. Detailed description of the preferred embodiments.**

[038] As already mentioned hereinbefore, the present invention is directed to a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone

belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC) type vector.

[039] For this purpose, the inventors have constructed several BAC-based mycobacterial genomic DNA libraries that may be used in order to perform the above described method.

[040] Because it is the first time that mycobacterial genomic DNA has been successfully cloned in BAC type vectors, and because these DNA libraries are then novel and nonobvious, an object of the present invention consists in a mycobacterial genomic DNA library cloned in such a BAC type vector.

[041] As an illustrative example, a BAC-based DNA library of *Mycobacterium tuberculosis* has been realized. Forty-seven cosmids chosen from the integrated map of the 4.4 Mb circular chromosome (Philipp et al., 1996a) were shotgun-sequenced during the initial phase of the H37Rv genome sequence project. The sequences of these clones were used as landmarks in the construction of a minimally overlapping BAC map. Comparison of the sequence data from the termini of 420 BAC clones allowed us to establish a minimal overlapping BAC map and to fill in the existing gaps between the sequence of cosmids. As well as using the BAC library for genomic mapping and sequencing, we also tested the system in comparative genomic experiments in order to uncover differences between two closely related mycobacterial species. As shown in a previous study (Philipp et al., 1996b), *M. tuberculosis*, *M. bovis* and *M. bovis* BCG, specifically BCG Pasteur strain, exhibit a high level of global genomic conservation, but certain polymorphic regions were also detected. Therefore, it was of great interest to find a reliable, easy and rapid way to exactly localize polymorphic regions in mycobacterial genomes using selected BAC clones. This approach was validated by determining the exact size and location of the polymorphisms in the genomic region of *DraI* fragment Z4 (Philipp et al., 1996b), taking advantage of the availability of an appropriate BAC clone covering the polymorphic region and the H37Rv genome sequence data. This region is located approximately 1.7 Mb from the origin of replication.

[042] The Bacterial Artificial Chromosome (BAC) cloning system is capable of stably propagating large, complex DNA inserts in *Escherichia coli*. As part of the *Mycobacterium tuberculosis* H37Rv genome sequencing project, a BAC library was constructed in the pBeloBAC11 vector and used for genome mapping, confirmation of sequence assembly, and sequencing. The library contains about 5000 BAC clones, with inserts ranging in size from 25 to 104 kb, representing theoretically a 70 fold coverage of

the *M. tuberculosis* genome (4.4 Mb). A total of 840 sequences from the T7 and SP6 termini of 420 BACs were determined and compared to those of a partial genomic database. These sequences showed excellent correlation between the estimated sizes and positions of the BAC clones and the sizes and positions of previously sequenced cosmids and the resulting contigs. Many BAC clones represent linking clones between sequenced cosmids, allowing full coverage of the H37Rv chromosome, and they are now being shotgun-sequenced in the framework of the H37Rv sequencing project. Also, no chimeric, deleted or rearranged BAC clones were detected, which was of major importance for the correct mapping and assembly of the H37Rv sequence. The minimal overlapping set contains 68 unique BAC clones and spans the whole H37Rv chromosome with the exception of a single gap of ~ 150 kb. As a post-genomic application, the canonical BAC set was used in a comparative study to reveal chromosomal polymorphisms between *M. tuberculosis*, *M. bovis* and *M. bovis* BCG Pasteur, and a novel 12.7 kb segment present *M. tuberculosis* but absent from *M. bovis* and *M. bovis* BCG was characterized. This region contains a set of genes whose products show low similarity to proteins involved in polysaccharide biosynthesis. The H37Rv BAC library therefore provides the one skilled in the art with a powerful tool both for the generation and confirmation of sequence data as well as for comparative genomics and a plurality of post-genomic applications.

[043] The above described BAC-based *Mycobacterium tuberculosis* genomic DNA library is part of the present invention and has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on November 19, 1997 under the accession number 1-1945.

[044] Another BAC-based DNA library has been constructed with the genomic DNA of *Mycobacterium bovis* BCG, Pasteur strain, and said DNA library has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on June 30, 1998 under the accession number I-2049.

[045] Thus, as a specific embodiment of the above described method for isolating a polynucleotide of interest said method makes use of at least one BAC-based DNA library that has been constructed from the genomic DNA of *Mycobacterium tuberculosis*, more specifically of the H37Rv strain and particularly of the DNA library deposited in the accession number 1-1945.

[046] In another specific embodiment of the above described method for isolating a polynucleotide of interest said method makes use of at least one BAC-based

DNA library has been constructed from the genomic DNA of *Mycobacterium bovis* BCG, more specifically of the Pasteur strain and particularly of the DNA library deposited in the accession number I-2049.

[047] In more details, the method according to the invention for isolating a polynucleotide of interest may comprise the following steps :

[048] a) isolating at least one polynucleotide contained in a clone of a BAC-based DNA library of mycobacterial origin;

[049] b) isolating:

[050] - at least one genomic or cDNA polynucleotide from a mycobacterium, said mycobacterium belonging to a strain different from the strain used to construct the BAC-based DNA library of step a); or alternatively

[051] - at least one polynucleotide contained in a clone of a BAC-based DNA library prepared from the genome of a mycobacterium that is different from the mycobacterium used to construct the BAC-based DNA library of step a);

[052] c) hybridizing the at least one polynucleotide of step a) to the at least one polynucleotide of step b);

[053] d) selecting the at least one polynucleotide of step a) that has not formed a hybrid complex with the at least one polynucleotide of step b);

[054] e) characterizing the selected polynucleotide.

[055] Following the above procedure, the at least one polynucleotide of step a) may be prepared as follows :

[056] 1) digesting at least one recombinant BAC clone by an appropriate restriction endonuclease in order to isolate the polynucleotide insert of interest from the vector genetic material;

[057] 2) optionally amplifying the resulting polynucleotide insert;

[058] 3) optionally digesting the polynucleotide insert of step 1) or step 2) with at least one restriction endonuclease.

[059] The above method of the invention allows the one skilled in the art to perform comparative genomics between different strains or species of mycobacteria cells, for example between pathogenic strains or species and their non pathogenic strains or species counterparts, as it is the illustrative case for the genomic comparison between *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG that is described herein in the examples.

[060] Restriction digests of a given clone of a BAC library according to the invention may be blotted to membranes, and then probed with radiolabeled DNA from another strain or another species of mycobacteria, allowing the one skilled in the art to identify, characterize and isolate a polynucleotide of interest that may be involved in important metabolic and/or physiological pathways of the mycobacterium under testing, such as a polynucleotide functionally involved in the pathogenicity of said given mycobacteria for its host organism.

[061] More specifically, the inventors have shown in Example 6 that when restriction digests of a given clone of the BAC library identified by the CNCM accession number 1-1945 are blotted to membranes and then probed with radiolabeled total genomic DNA from, for example, *Mycobacterium bovis* BCG Pasteur, it is observed that restriction fragments that fail to hybridize with the *M. bovis* BCG Pasteur DNA are absent from its genome, hence identifying polymorphic regions between *M. bovis* BCG Pasteur and *M. tuberculosis* H37Rv.

[062] Thus, a further object of the present invention consists in a polynucleotide of interest that has been isolated according to the method described herein before.

[063] In Example 6, a polynucleotide of approximately 12.7 kilobases has been isolated that is present in the genome of *M. tuberculosis* but is absent of the genome of *M. bovis* BCG. This polynucleotide of interest contains 11 ORFs that may be involved in polysaccharide biosynthesis. In particular, two of said ORFs are of particular interest namely ORF6 (MTCY277.33; Rv1511) that encodes a protein that shares significant homology with bacterial GDP-D-mannose dehydratases, whereas the protein encoded by ORF7 (MTCY277.34; Rv1512) shares significant homology with a nucleotide sugar epimerase. As polysaccharide is a major constituent of the mycobacterial cell wall, these deleted genes may cause the cell wall of *M. bovis* BCG to differ from that of *M. tuberculosis*, a fact that may have important consequences for both the immune response to *M. bovis* BCG and virulence. Detection of such a polysaccharide is of diagnostic interest and possibly useful in the design of tuberculosis vaccines.

[064] Consequently, the polynucleotide of interest obtained following the method according to the invention may contain at least one ORF, said ORF preferably encoding all or part of a polypeptide involved in an important metabolic and/or physiological pathway of the mycobacteria under testing, and more specifically all or part of a polypeptide that is involved in the pathogenicity of the mycobacteria under testing,

such as for example *Mycobacterium tuberculosis*, and more generally mycobacteria belonging to the *Mycobacterium tuberculosis* complex.

[065] The *Mycobacterium tuberculosis* complex has its usual meaning, i.e. the complex of mycobacteria causing tuberculosis which are *Mycobacterium tuberculosis*, *Mycobacterium bovis*, *Mycobacterium africanum*, *Mycobacterium microti* and the vaccine strain *Mycobacterium bovis* BCG.

[066] An illustrative polynucleotide of interest according to the present invention comprises all or part of the polynucleotide of approximately 12.7 kilobases that is present in the genome of *M. tuberculosis* but is absent from the genome of *M. bovis* BCG disclosed hereinbefore. This polynucleotide is contained in clone Rv58 of the BAC DNA library I-1945.

[067] Generally, the invention also pertains to a purified polynucleotide comprising the DNA insert contained in a recombinant BAC vector belonging to a BAC-based mycobacterial genomic DNA library, such as for example the I-1945 BAC DNA library.

[068] Advantageously, such a polynucleotide has been identified according to the method of the invention.

[069] Such a polynucleotide of interest may be used as a probe or a primer useful for specifically detecting a given mycobacterium of interest, such as *Mycobacterium tuberculosis* or *Mycobacterium bovis* BCG.

[070] More specifically, the invention then deals with a purified polynucleotide useful as probe or a primer comprising all or part of the nucleotide sequence SEQ ID N° 1.

[071] The location, on the *Mycobacterium tuberculosis* chromosome, of the above polynucleotide of sequence SEQ ID N° 1 has now been ascribed to begin, at its 5' end at nucleotide at position nt 1696015 and to end, at its 3' end, at nucleotide at position nt 1708746.

[072] For diagnostic purposes, this 12.7 kb deletion should allow a rapid PCR screening of tubercle isolates to identify whether they are bovine or human strains. The primers listed in Table I are flanking the deleted region and give a 722 bp amplicon in *M. bovis* or *M. bovis* BCG strains, but a fragment of 13,453 bp in *M. tuberculosis* that is practically impossible to amplify under the same PCR conditions. More importantly, assuming that some of the gene products from this region represent proteins with antigenic properties, it could be possible to develop a test that can reliably distinguish

between the immune response induced by vaccination with *M. bovis* BCG vaccine strains and infection with *M. tuberculosis* or that the products (e.g. polysaccharides) are specific immunogens.

[073] The invention also provides for a purified polynucleotide useful as a probe or as a primer, said polynucleotide being chosen in the following group of polynucleotides :

[074] a) a polynucleotide comprising at least 8 consecutive nucleotides of the sequence SEQ ID N° 1;

[075] b) a polynucleotide whose sequence is fully complementary to the sequence of the polynucleotide defined in a);

[076] c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

[077] For the purpose of defining a polynucleotide or oligonucleotide hybridizing under stringent hybridization conditions, such as above, it is intended a polynucleotide that hybridizes with a reference polynucleotide under the following hybridization conditions.

[078] The hybridization step is realized at 65°C in the presence of 6 x SSC buffer, 5 x Denhardt's solution, 0,5% SDS and 100µg/ml of salmon sperm DNA.

[079] For technical information, 1 x SSC corresponds to 0.15 M NaCl and 0.05M sodium citrate; 1 x Denhardt's solution corresponds to 0.02% Ficoll, 0.02% polyvinylpyrrolidone and 0.02% bovine serum albumin.

[080] The hybridization step is followed by four washing steps :

[081] - two washings during 5 min, preferably at 65°C in a 2 x SSC and 0.1% SDS buffer,

[082] - one washing during 30 min, preferably at 65°C in a 2 x SSC and 0.1% SDS buffer,

[083] - one washing during 10 min, preferably at 65°C in a 0.1 x SSC and 0.1%SDS buffer.

[084] A first illustrative useful polynucleotide that is included in the polynucleotide of sequence SEQ ID N°1 is the polynucleotide of sequence SEQ ID N°2 that corresponds to the Sp6 end-sequence of SEQ ID N°1.

[085] A second illustrative useful polynucleotide that is included in the polynucleotide of sequence SEQ ID N°1 is the polynucleotide of sequence SEQ ID N°3 that corresponds to the T7 end-sequence of SEQ ID N°1, located on the opposite strand.

[086] The polynucleotide of sequence SEQ ID N°1 contains 11 ORFs, the respective locations of which, taking into account the orientation of each ORF on the chromosome, on the sequence of the *Mycobacterium tuberculosis* chromosome, is given hereafter:

[087] - The location of ORF1 is comprised between nucleotide at position nt 1695944 and nucleotide at position nt 1696441.

[088] - The location of ORF2 is comprised between nucleotide at position nt 1696728 and nucleotide at position nt1697420.

[089] - The location of ORF3 is comprised between nucleotide at position nt 1698096 and nucleotide at position nt1699892. ORF3 probably encodes a protein having the characteristics of a membrane protein.

[090] - The location of ORF4 is comprised between nucleotide at position nt 1700210 and nucleotide at position nt1701088.

[091] - The location of ORF5 is comprised between nucleotide at position nt 1701293 and nucleotide at position nt1702588. ORF5 encodes a protein having the characteristics of a membrane protein.

[092] - The location of ORF6 is comprised between nucleotide at position nt 1703072 and nucleotide at position nt1704091. ORF6 encodes a protein having the characteristics of a GDP-D-mannose dehydratase.

[093] - The location of ORF7 is comprised between nucleotide at position nt 1704091 and nucleotide at position nt1705056. ORF7 encodes a protein having the characteristics of a nucleotide sugar epimerase involved in colanic acid biosynthesis.

[094] - The location of ORF8 is comprised between nucleotide at position nt 1705056 and nucleotide at position nt1705784.

[095] - The location of ORF9 is comprised between nucleotide at position nt 1705808 and nucleotide at position nt1706593. ORF9 encodes a protein having the characteristics of colanic acid biosynthesis glycosyl transferase.

[096] - The location of ORF10 is comprised between nucleotide at position nt 1706631 and nucleotide at position nt 1707524.



[097] - The location of ORF11 is comprised between nucleotide at position nt 1707530 and nucleotide at position nt1708648. ORF11 encodes a protein similar to a spore coat polysaccharide biosynthesis.

[098] A polynucleotide of interest obtained by the above-disclosed method according to the invention may also contain at least one ORF that encodes all or part of acidic, glycine-rich proteins, belonging to the PE and PPE families, whose genes are often clustered and based on multiple copies of the polymorphic repetitive sequences. The names PE and PPE derive from the fact that the motifs ProGlu (PE, positions 8, 9) and ProProGlu (PPE, positions 7 to 9) are found near the N-terminus in almost all cases. The PE protein family all have a highly conserved N-terminal domain of ~110 amino acid residues, that is predicted to have a globular structure, followed by a C-terminal segment which varies in size, sequence and repeat copy number. Phylogenetic analysis separated the PE family into several groups, the larger of which is the highly repetitive PGRS class containing 55 members whereas the other groups share very limited sequence similarity in their C-terminal domains. The predicted molecular weights of the PE proteins vary considerably as a few members only contain the ~110 amino acid N-terminal domain while the majority have C-terminal extensions ranging in size from 100 up to >1400 residues. A striking feature of the PGRS proteins is their exceptional glycine content (up to 50%) due to the presence of multiple tandem repetitions of GlyGlyAla or GlyGlyAsn motifs or variations thereof.

[099] Like the PE family, the PPE protein family also has a conserved N-terminal domain that comprises ~180 amino acid residues followed by C-terminal segments that vary considerably in sequence and length. These proteins fall into at least three groups, one of which constitutes the MPTR class characterised by the presence of multiple, tandem copies of the motif AsnXGlyXGlyAsnXGly (SEQ ID NO. 730). The second subgroup contains a characteristic, well-conserved motif around position 350 (GlyXXSerValProXXTrp)(SEQ ID NO. 731), whereas the other group contains proteins that are unrelated except for the presence of the common 180-residue PPE domain. C-terminal extensions may range in size from 00 up to 3500 residues.

[0100] One member of the PGRS sub-family, the WHO antigen 22T (Abou-Zeid et al., 1991), a 55kD protein capable of binding fibronectin, is produced during disease and elicits a variable antibody response suggesting either that individuals mount different immune responses or that this PGRS-protein may not be produced in this form by all strains of *M. tuberculosis*. In other words, at least some PE\_PGRS coding sequences

encode for proteins that are involved in the recognition of *M. tuberculosis* by the immune system of the infected host. Therefore, differences in the PGRS sequences could represent the principal source of antigenic variation in the otherwise genetically and antigenically homogeneous bacterium.

[0101] By performing the method of the invention using the *M. tuberculosis* BAC based DNA library I-1945, the inventors have discovered the occurrence of sequence differences between a given PGRS encoding ORF (ORF reference on the genomic sequence of *M. tuberculosis* Rv0746) of *M. tuberculosis* and its counterpart sequence in the genome of *M. bovis* BCG.

[0102] More precisely, the inventors have determined that one ORF contained in BAC vector N° Rv418 of the *M. tuberculosis* BCG I-1945 DNA library carries both base additions and base deletions when compared with the corresponding ORF in the genome of *M. bovis* BCG that is contained in the BAC vector N° X0175 of the *M. bovis* BCG I-2049 DNA library. The variations observed in the base sequences correspond to variations in the C-terminal part of the aminoacid sequence of the PGRS ORF translation product.

[0103] As shown in Figure 6, an amino acid stretch of 9 residues in length is present in this *M. tuberculosis* PGRS (ORF reference Rv0746) and is absent from the ORF counterpart of *M. bovis* BCG, namely the following amino acid sequence:

[0104] NH<sub>2</sub>-GGAGGAGGSSAGGGGAGGAGGAGGWLLGD-COOH (SEQ ID NO. 732).

[0105] Furthermore, Figure 6 shows also that an amino acid stretch of 45 residues in length is absent from this *M. tuberculosis* PGRS and is present in the ORF counterpart of *M. bovis* BCG, namely following amino acid sequence:

[0106] NH<sub>2</sub>-GAGGIGGIGGNANGGAGGNGGTGGQLWGSGGAGVEGGAAL SVGDT-COOH (SEQ ID NO. 733).

[0107] Similar observations were made with PPE ORF Rv0442, which showed a 5 codon deletion relative to a *M. bovis* amino acid sequence.

[0108] Given that the polymorphism associated with the PE-PGRS or PEE ORFS resulted in extensive antigenic variability or reduced antigen presentation, this would be of immense significance for vaccine design, for understanding protective immunity in tuberculosis and, possibly, explain the varied responses seen in different BCG vaccination programmes.

[0109] There are several striking parallels between the PGRS proteins and the Epstein-Barr virus-encoded nuclear antigens (EBNA). Both polypeptide families are

glycine-rich, contain Gly-Ala repeats that represent more than one third of the molecule, and display variation in the length of the repeat region between different isolates. The Gly-Ala repeat region of EBNA1 has been shown to function as a *cis*-acting inhibitor of antigen processing and MHC class I-restricted antigen presentation. (Levitskaya et al., 1995). The fact that MHC class I knock-out mice are extremely susceptible to *M. tuberculosis* underlines the importance of MHC class I antigen presentation in protection against tuberculosis. Therefore, it is possible that the PE/PPE protein family also play some role in inhibiting antigen presentation, allowing the bacillus to hide from the host's immune system.

[0110] As such the novel and nonobvious PGRS polynucleotide from *M. bovis* which is homolog to the *M. tuberculosis* ORF Rv0746, and which is contained in the BAC clone N° X0175 (See Table 4 for SP6 and T7 end-sequences of clone n° X0175) of the I-2049 *M. bovis* BCG BAC DNA library is part of the present invention, as it represents a starting material in order to define specific probes or primers useful for detection of antigenic variability in mycobacterial strains, possible inhibition of antigen processing as well as to differentiate *M. tuberculosis* from *M. bovis* BCG.

[0111] Thus, a further object of the invention consists in a polynucleotide comprising the sequence SEQ ID N°4.

[0112] Polynucleotides of interest have been defined by the inventors as useful detection tools in order to differentiate *M. tuberculosis* from *M. bovis* BCG. Such polynucleotides are contained in the 45 aminoacid length coding sequence that is present in *M. bovis* BCG but absent from *M. tuberculosis*. This polynucleotide has a sequence beginning (5' end) at the nucleotide at position nt 729 of the sequence SEQ ID N°4 and ending (3' end) at the nucleotide in position nt 863 of the sequence SEQ ID N°4.

[0113] Thus, part of the present invention is also a polynucleotide which is chosen among the following group of polynucleotides :

[0114] a) a polynucleotide comprising at least 8 consecutive nucleotides of the nucleotide sequence SEQ ID N°5 ;

[0115] b) a polynucleotide which sequence is fully complementary to the sequence of the polynucleotide defined in a) ;

[0116] c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

[0117] The stringent hybridization conditions for the purpose of defining the above disclosed polynucleotide are defined herein before in the specification.

[0118] The invention also provides for a BAC-based *Mycobacterium tuberculosis* strain H37Rv genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes on November 19, 1997 under the accession number I-1945.

[0119] A further object of the invention consists in a recombinant BAC vector which is chosen among the group consisting of the recombinant BAC vectors belonging to the BAC-based DNA library I-1945.

[0120] Generally, a recombinant BAC vector of interest may be chosen among the following set or group of BAC vectors contained in the BAC-based DNA library I-1945 :

[0121] Rv101; Rv102; Rv103; Rv104; Rv105; Rv106; Rv107; Rv108; Rv109; Rv110; Rv111; Rv112; Rv113; Rv114; Rv115; Rv116; Rv117; Rv118; Rv119; Rv120; Rv121; Rv122; Rv123; Rv124; Rv126; Rv127; Rv128; Rv129; Rv130; Rv132; Rv134; Rv135; Rv136; Rv137; Rv138; Rv139; Rv140; Rv141; Rv142; Rv143; Rv144; Rv145; Rv146; Rv147; Rv148; Rv149; Rv150; Rv151; Rv152; Rv153; Rv154; Rv155; Rv156; Rv157; Rv159; Rv160; Rv161; Rv162; Rv163; Rv164; Rv165; Rv166; Rv167; Rv169; Rv170; Rv171; Rv172; Rv173; Rv174; Rv175; Rv176; Rv177; Rv178; Rv179; Rv180; Rv181; Rv182; Rv183; Rv184; Rv185; Rv186; Rv187; Rv188; Rv189; Rv190; Rv191; Rv192; Rv193; Rv194; Rv195; Rv196; Rv197; Rv198; Rv199; Rv200; Rv201; Rv204; Rv205; Rv207; Rv209; Rv210; Rv214; Rv215; Rv217; Rv218; Rv219; Rv220; Rv221; Rv222; Rv223; Rv224; Rv225; Rv226; Rv227; Rv228; Rv229; Rv230; Rv231; Rv232; Rv233; Rv234; Rv235; Rv237; Rv240; Rv241; Rv243; Rv244; Rv245; Rv246; Rv247; Rv249; Rv250; Rv251; Rv252; Rv253; Rv254; Rv255; Rv257; Rv258; Rv259; Rv260; Rv261; Rv262; Rv263; Rv264; Rv265; Rv266; Rv267; Rv268; Rv269; Rv270; Rv271; Rv272; Rv273; Rv274; Rv275; Rv276; Rv277; Rv278; Rv279; Rv280; Rv281; Rv282; Rv283; Rv284; Rv285; Rv286; Rv287; Rv288; Rv289; Rv290; Rv291; Rv292; Rv293; Rv294; Rv295; Rv296; Rv297; Rv298; Rv299; Rv300; Rv301; Rv302; Rv303; Rv304; Rv306; Rv307; Rv308; Rv309; Rv310; Rv311; Rv312; Rv313; Rv314; Rv315; Rv316; Rv317; Rv318; Rv319; Rv320; Rv321; Rv322; Rv327; Rv328; Rv329; Rv330; Rv331; Rv333; Rv334; Rv335; Rv336; Rv337; Rv338; Rv339; Rv340; Rv341; Rv343; Rv344; Rv346; Rv347; Rv348; Rv349; Rv350; Rv351; Rv352; Rv353; Rv354; Rv355; Rv356; Rv357; Rv358; Rv359; Rv360; Rv361; Rv363; Rv364; Rv365; Rv366; Rv367; Rv368; Rv369; Rv370; Rv371; Rv373; Rv374; Rv375; Rv376; Rv377; Rv378; Rv379; Rv380; Rv381; Rv382; Rv383; Rv384; Rv385; Rv386; Rv387; Rv388;

Rv389; Rv38; Rv390; Rv391; Rv392; Rv393; Rv396; Rv39; Rv3; Rv40; Rv412; Rv413; Rv414; Rv415; Rv416; Rv417; Rv418; Rv419; Rv41; Rv42; Rv43; Rv44; Rv45; Rv46; Rv47; Rv48; Rv49; Rv4; Rv50; Rv51; Rv52; Rv53; Rv54; Rv55; Rv56; Rv57; Rv58; Rv59; Rv5; Rv60; Rv61; Rv62; Rv63; Rv64; Rv65; Rv66; Rv67; Rv68; Rv69; Rv6; Rv70; Rv71; Rv72; Rv73; Rv74; Rv75; Rv76; Rv77; Rv78; Rv79; Rv7; Rv80; Rv81; Rv82; Rv83; Rv84; Rv85; Rv86; Rv87; Rv88; Rv89; Rv8; Rv90; Rv91; Rv92; Rv94; Rv95; Rv96; Rv9.

[0122] The end sequences of the polynucleotide inserts of each of the above clones corresponding respectively to the sequences adjacent to the T7 promoter and to the Sp6 promoter on the BAC vector are shown in Table 3.

[0123] It has been shown by the inventors that the minimal overlapping set of BAC vectors of the BAC-based DNA library I-1945 contains 68 unique BAC clones and practically spans almost the whole H37Rv chromosome with the exception of a single gap of approximately 150 kb.

[0124] More specifically, a recombinant BAC vector of interest is chosen among the following set or group of BAC vectors from the BAC-based DNA library I-1945, the location of which vector DNA inserts on the chromosome of *M. tuberculosis* is shown in Figure 3 :

[0125] Rv234; Rv351; Rv166; Rv35; Rv415; Rv404; Rv209; Rv272; Rv30; Rv228; Rv233; Rv38; Rv280; Rv177; Rv48; Rv374; Rv151; Rv238; Rv156; Rv92; Rv3; Rv403; Rv322; Rv243; Rv330; Rv285; Rv233; Rv219; Rv416; Rv67; Rv222; Rv149; Rv279; Rv87; Rv273; Rv266; Rv25; Rv136; Rv414; Rv13; Rv289; Rv60; Rv104; Rv5; Rv165; Rv215; Rv329; Rv240; Rv19; Rv74; Rv411; Rv167; Rv56; Rv80; Rv164; Rv59; Rv313; Rv265; Rv308; Rv220; Rv258; Rv339; Rv121; Rv419; Rv418; Rv45; Rv217; Rv134; Rv17; Rv103; Rv21; Rv22; Rv2; Rv270; Rv267; Rv174; Rv257; Rv44; Rv71; Rv7; Rv27; Rv191; Rv230; Rv128; Rv407; Rv106; Rv39; Rv255; Rv74; Rv355; Rv268; Rv58; Rv173; Rv264; Rv417; Rv401; Rv144; Rv302; Rv81; Rv163; Rv281; Rv221; Rv420; Rv175; Rv86; Rv412; Rv73; Rv269; Rv214; Rv287; Rv42; Rv143.

[0126] The polynucleotides disclosed in Table 3 may be used as probes in order to select a given clone of the BAC DNA library I-1945 for further use.

[0127] The invention also provides for a BAC-based *Mycobacterium bovis* strain Pasteur genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes on June 30, 1998 under the accession number I-2049.

[0128] A further object of the invention consists in a recombinant BAC vector which is chosen among the group consisting of the recombinant BAC vectors belonging to the BAC-based DNA library I-2049. This DNA library contains approximately 1600 clones. The average insert size is estimated to be ~80 kb.

[0129] Generally, a recombinant BAC vector of interest may be chosen among the following set or group of BAC vectors contained in the BAC-based DNA library I-2049:

[0130] X0001; X0002; X0003; X0004; X0006; X0007; X0008; X0009; X0010; X0012; X0013; X0014; X0015; X0016; X0017; X0018; X0019; X0020; X0021; X0175.

[0131] The end sequences of the polynucleotide inserts of each of the above clones corresponding respectively to the sequences adjacent to the T7 promoter and to the Sp6 promoter on the BAC vector are shown in Table 4.

[0132] The polynucleotides disclosed in Table 4 may be used as probes in order to select a given clone of the BAC DNA library I-2049 for further use.

[0133] Are also part of the invention the polynucleotide inserts that are contained in the above described BAC vectors, that are useful as primers or probes.

[0134] These polynucleotides and nucleic acid fragments may be used as primers for use in amplification reactions, or as nucleic probes.

[0135] PCR is described in the US patent N° 4,683,202. The amplified fragments may be identified by an agarose or a polyacrylamide gel electrophoresis, or by a capillary electrophoresis or alternatively by a chromatography technique (gel filtration, hydrophobic chromatography or ion exchange chromatography). The specificity of the amplification may be ensured by a molecular hybridization using, for example, one of the initial primers as nucleic probes.

[0136] Amplified nucleotide fragments are used as probes in hybridization reactions in order to detect the presence of one polynucleotide according to the present invention or in order to detect mutations in the genome of the given mycobacterium of interest, specifically a mycobacterium belonging to the *Mycobacterium tuberculosis* complex and more specifically *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG.

[0137] Are also part of the present invention the amplified nucleic fragments («amplicons») defined herein above.

[0138] These probes and amplicons may be radioactively or non-radioactively labeled, using for example enzymes or fluorescent compounds.

[0139] Other techniques related to nucleic acid amplification may also be used and are generally preferred to the PCR technique.

[0140] The Strand Displacement Amplification (SDA) technique (Walker et al., 1992) is an isothermal amplification technique based on the ability of a restriction enzyme to cleave one of the strands at his recognition site (which is under a hemiphosphorothioate form) and on the property of a DNA polymerase to initiate the synthesis of a new strand from the 3'OH end generated by the restriction enzyme and on the property of this DNA polymerase to displace the previously synthesized strand being localized downstream. The SDA method comprises two main steps:

[0141] a) The synthesis, in the presence of dCTP-alpha-S, of DNA molecules that are flanked by the restriction sites that may be cleaved by an appropriate enzyme.

[0142] b) The exponential amplification of these DNA molecules modified as such, by enzyme cleavage, strand displacement and copying of the displaced strands. The steps of cleavage, strand displacement and copy are repeated a sufficient number of times in order to obtain an accurate sensitivity of the assay.

[0143] The SDA technique was initially realized using the restriction endonuclease HincII but is now generally practised with an endonuclease from *Bacillus stearothermophilus* (BSOBI) and a fragment of a DNA polymerase which is devoid of any 5'→3'exonuclease activity isolated from *Bacillus cladothecae* (exo- Bca) [=exo-minus-Bca]. Both enzymes are able to operate at 60°C and the system is now optimized in order to allow the use of dUTP and the decontamination by UDG. When using this technique, as described by Spargo et al. in 1996, the doubling time of the target DNA is of 26 seconds and the amplification rate is of  $10^{10}$  after an incubation time of 15 min at 60°C.

[0144] The SDA amplification technique is more easy to perform than PCR (a single thermostated waterbath device is necessary) and is faster than the other amplification methods.

[0145] Thus, another object of the present invention consists in using the nucleic acid fragments according to the invention (primers) in a method of DNA or RNA amplification according to the SDA technique. For performing SDA, two pairs of primers are used : a pair of external primers (B1, B2) consisting of a sequence specific for the target polynucleotide of interest and a pair of internal primers (S1, S2) consisting of a fusion oligonucleotide carrying a site that is recognized by a restriction endonuclease, for exemple the enzyme BSOBI.

[0146] The operating conditions to perform SDA with such primers are described in Spargo et al, 1996.

[0147] The polynucleotides of the invention and their above described fragments, especially the primers according to the invention, are useful as technical means for performing different target nucleic acid amplification methods such as:

[0148] - TAS (Transcription-based Amplification System), described by Kwoh et al. in 1989.

[0149] - SR (Self-Sustained Sequence Replication), described by Guatelli et al. in 1990.

[0150] - NASBA (Nucleic acid Sequence Based Amplification), described by Kievitis et al. in 1991.

[0151] - TMA (Transcription Mediated Amplification).

[0152] The polynucleotides according to the invention are also useful as technical means for performing methods for amplification or modification of a nucleic acid used as a probe, such as:

[0153] - LCR (Ligase Chain Reaction), described by Landegren et al. in 1988 and improved by Barany et al. in 1991 who employ a thermostable ligase.

[0154] - RCR (Repair Chain Reaction) described by Segev et al. in 1992.

[0155] - CPR (Cycling Probe Reaction), described by Duck et al. in 1990.

[0156] - Q-beta replicase reaction, described by Miele et al. in 1983 and improved by Chu et al. in 1986, Lizardi et al. in 1988 and by Burg et al. and Stone et al. in 1996.

[0157] When the target polynucleotide to be detected is a RNA, for example a mRNA, a reverse transcriptase enzyme will be used before the amplification reaction in order to obtain a cDNA from the RNA contained in the biological sample. The generated cDNA is subsequently used as the nucleic acid target for the primers or the probes used in an amplification process or a detection process according to the present invention.

[0158] The non-labeled polynucleotides or oligonucleotides of the invention may be directly used as probes. Nevertheless, the polynucleotides or oligonucleotides are generally labeled with a radioactive element ( $^{32}\text{P}$ ,  $^{35}\text{S}$ ,  $^3\text{H}$ ,  $^{125}\text{I}$ ) or by a nonisotopic molecule (for example, biotin, acetylaminofluorene, digoxigenin, 5bromodesoxyuridin, fluorescein) in order to generate probes that are useful for numerous applications.

[0159] Examples of non-radioactive labeling, of nucleic acid -fragments are described in the french patent N° FR-7810975 or by Urdea et al. or Sanchez-Pescador et al., 1988.



[0160] In the latter case, other labeling techniques may be also used such as those described in the french patents FR-2 422 956 and 2 518 755. The hybridization step may be performed in different ways (Matthews et al., 1988). The more general method consists of immobilizing the nucleic acid that has been extracted from the biological sample onto a substrate (nitrocellulose, nylon, polystyrene) and then to incubate, in defined conditions, the target nucleic acid with the probe. Subsequently to the hybridization step, the excess amount of the specific probe is discarded and the hybrid molecules formed are detected by an appropriate method (radioactivity, fluorescence or enzyme activity measurement).

[0161] Advantageously, the probes according to the present invention may have structural characteristics such that they allow the signal amplification, such structural characteristics being, for example, branched DNA probes as those described by Urdea et al. in 1991 or in the European patent N° EP-0 225 807 (Chiron).

[0162] In another advantageous embodiment of the probes according to the present invention, the latters may be used as « capture probes », and are for this purpose immobilized on a substrate in order to capture the target nucleic acid contained in a biological sample. The captured target nucleic acid is subsequently detected with a second probe which recognizes a sequence of the target nucleic acid which is different from the sequence recognized by the capture probe.

[0163] The oligonucleotide probes according to the present invention may also be used in a detection device comprising a matrix library of probes immobilized on a substrate, the sequence of each probe of a given length being localized in a shift of one or several bases, one from the other, each probe of the matrix library thus being complementary to a distinct sequence of the target nucleic acid. Optionally, the substrate of the matrix may be a material able to act as an electron donor, the detection of the matrix poisons in which an hybridization has occurred being subsequently determined by an electronic device. Such matrix libraries of probes and methods of specific detection of a targer nucleic acid is described in the European patent application N° EP-0 713 016 (Affymax technologies) and also in the US patent N° US-5,202,231 (Drmanac).

[0164] Since almost the whole length of a mycobacterial chromosme is covered by a BAC-based genomic DNA libraries according to the present invention (i.e. 97% of the *M. tuberculosis* chromosome is covered by the BAC library I-1945), these DNA libraries will play an important role in a plurality of post-genomic applications, such as in mycobacterial gene expression studies where the canonical set of BACs could be used as

a matrix for hybridization studies. Probing such matrices with cDNA probes prepared from total mRNA will uncover genetic loci induced or repressed under different physiological conditions (Chuang et al., 1993; Trieselmann et al., 1992). As such, the H37Rv BAC library represents a fundamental resource for present and future genomics investigations.

[0165] The BAC vectors or the polynucleotide inserts contained therein may be directly used as probes, for example when immobilized on a substrate such as described herein before.

[0166] The BAC vectors or their polynucleotide inserts may be directly adsorbed on a nitrocellulose membrane, at predetermined locations on which one or several polynucleotides to be tested are then put to hybridize therewith.

[0167] Preferably, a collection of BAC vectors that spans the whole genome of the mycobacterium under testing will be immobilized, such as, for example, the set of 68 BAC vectors of the I-1945 DNA library that is described elsewhere in the specification and shown in Figure 3.

[0168] The immobilization and hybridization steps may be performed as described in the present Materials and Methods Section.

[0169] As another illustrative embodiment of the use of the BAC vectors of the invention as polynucleotide probes, these vectors may be useful to perform a transcriptional activity analysis of mycobacteria growing in different environmental conditions, for example under conditions in which a stress response is expected, as it is the case at an elevated temperature, for example 40°C.

[0170] In this specific embodiment of the invention, Genescreen membranes may be used to immobilize the restriction endonuclease digests (*Hind*III digests for the BAC DNA library I-1945) of the BAC vectors by transfer from a gel (Trieselmann et al., 1992).

[0171] Alternatively, the BAC vectors may be immobilized for dot blot experiments as follows. First, the DNA concentration of each BAC clone is determined by hybridization of blots of clone DNAs and of a BAC vector concentration standard with a BAC vector specific DNA probe. Hybridization is quantified by the Betascope 603 blot analyzer (Betagen Corp.), which collects beta particles directly from the blot with high efficiency. Then, 0.5 µg of each clone DNA is incubated in 0.25 M NaOH and 10 mM EDTA at 65°C for 60 min to denature the DNA and degrade residual RNA contaminants. By using a manifold filtration system (21 by 21 wells), each clone DNA is blotted onto a GeneScreen Plus nylon membrane in the alkaline solution. After neutralization, the blots

are baked at 85°C for 2 h under vacuum. Positive and negative controls are added when necessary. In order to perform this procedure, it may be referred to the article of Chuang et al. (1993).

[0172] For RNA extractions, cells grown in a suitable volume of culture medium may, for example, be immediately mixed with an equal volume of crushed ice at -70°C and spun at 4°C in a 50 ml centrifugation tube. The cell pellet is then suspended in 0.6 ml of ice-cold buffer (10 mM KCl, 5 mM MgCl, 10 mM Tris; pH 7.4) and then immediately added to 0.6 ml of hot lysis buffer (0.4 M NaCl, 40 mM EDTA, 1% beta-mercaptoethanol, 1% SDS, 20 mM Tris; pH 7.4) containing 100 µl of water saturated phenol. This mixture is incubated in a boiling water bath for 40 s. The debris are removed by centrifugation. The supernatant is extracted with phenol-chloroform five times, ethanol precipitated, and dried. The dried RNA pellet is dissolved in water before use.

[0173] Then labeled total cDNA may be prepared by the following method. The reaction mixture contains 15 µg of the previously prepared total RNA, 5 µg of pd(N<sub>6</sub>) (random hexamers from Pharmacia Inc.), 0.5 mM dATP, 0.5 mM dGTP and 0.5mM DTTP, 5µM dCTP, 100 µCi of [ $\alpha$ -<sup>32</sup>P]dCTP (3,000 Ci/mmol), 50 mM Tris-HCl (pH 8.3), 6 mM MgCl<sub>2</sub>, 40 mM KCl, 0.5 U of avian myeloblastosis virus reverse transcriptase (Life Science Inc.) in a total volume of 50 µl. The reaction is allowed to continue overnight at room temperature. EDTA and NaOH are then added to final concentrations of 50 mM and 0.25 M, respectively, and the mixture is incubated at 65°C for 30 min to degrade the RNA templates. The cDNA is then ready to use after neutralization by adding Hcl and Tris buffer.

[0174] The hybridization step may be performed as described by Chuang et al. (1993) and briefly disclosed hereinafter. The DNA dot blot is hybridized to <sup>32</sup>P- labeled total cDNA in a solution containing 0.1% polyvinylpyrrolidone, 0.1% Ficoll 0.1% sodium Ppi, 0.1% bovine serum albumin, 0.5% SDS, 100 mM NaCl, and 0.1 mM sodium citrate, pH 7.2, at 65°C for 2 days and then washed with a solution containing 0.1% SDS, 100 mM NaCl, and 10 mM Na-citrate, pH 7.2. The same dot blot is used for hybridization with both control and experimental cDNAs, with an alkaline probe stripping procedure (soaked twice in 0.25M NaOH-0.75 M NaCl at room temperature, 30 min each, neutralized, and completely dried at 65°C for at least 30 min) between the two hybridizations. Quantification may be done with the Betascope 603 blot analyzer (Betagen Corp.).

[0175] As it flows from the above technical teachings, another object of the invention consists in a method for detecting the presence of mycobacteria in a biological sample comprising the steps of:

[0176] a) bringing into contact the recombinant BAC vector or a purified polynucleotide according to the invention with a biological sample ;

[0177] b) detecting the hybrid nucleic acid molecule formed between said purified polynucleotide and the nucleic acid molecules contained within the biological sample.

[0178] The invention further deals with a method for detecting the presence of mycobacteria in a biological sample comprising the steps of:

[0179] a) bringing into contact the recombinant BAC vector or a purified polynucleotide according to the invention that has been immobilized onto a substrate with a biological sample;

[0180] b) bringing into contact the hybrid nucleic acid molecule formed between said purified polynucleotide and the nucleic acid contained in the biological sample with a labeled recombinant BAC vector or a polynucleotide according to the invention, provided that said polynucleotide and polynucleotide of step a) have non-overlapping sequences.

[0181] Another object of the invention consists in a method for detecting the presence of mycobacteria in a biological sample comprising the steps of:

[0182] a) bringing into contact the nucleic acid molecules contained in the biological sample with a pair of primers according to the invention;

[0183] b) amplifying said nucleic acid molecules;

[0184] c) detecting the nucleic acid fragments that have been amplified, for example by gel electrophoresis or with a labeled polynucleotide according to the invention.

[0185] In one specific embodiment of the above detection and/or amplification methods, said methods comprise an additional step wherein before step a), the nucleic acid molecules of the biological sample have been made available to a hybridization reaction.

[0186] In another specific embodiment of the above detection methods, said methods comprise an additional step, wherein, before the detection step, the nucleic acid molecules that are not hybridized with the immobilized purified polynucleotide are removed.

[0187] Also part of the invention is a kit for detecting mycobacteria in a biological sample comprising:

[0188] a) a recombinant BAC vector or a purified polynucleotide according to the invention;

[0189] b) reagents necessary to perform a nucleic acid hybridization reaction.

[0190] The invention also pertains to a kit for detecting a mycobacteria in a biological sample comprising:

[0191] a) a recombinant BAC vector or a purified polynucleotide according to the invention that is immobilized onto a substrate;

[0192] b) reagents necessary to perform a nucleic acid hybridization reaction;

[0193] c) a purified polynucleotide according to the invention which is radioactively or non-radioactively labeled, provided that said polynucleotide and the polynucleotide of step a) have non-overlapping sequences.

[0194] Moreover, the invention provides for a kit for detecting mycobacteria in a biological sample comprising:

[0195] a) a pair of purified primers according to the invention;

[0196] b) reagents necessary to perform a nucleic acid amplification reaction;

[0197] c) optionally, a purified polynucleotide according to the invention useful as a probe.

[0198] The invention embraces also a method for detecting the presence of a genomic DNA, a cDNA or a mRNA of mycobacteria in a biological sample, comprising the steps of :

[0199] a) bringing into contact the biological sample with a plurality of BAC vectors according to the invention or purified polynucleotides according to the invention, that are immobilized on a substrate;

[0200] b) detecting the hybrid complexes formed.

[0201] The invention also provides a kit for detecting the presence of genomic DNA, cDNA or mRNA of a mycobacterium in a biological sample, comprising:

[0202] a) a substrate on which a plurality of BAC vectors according to the invention or purified polynucleotides according to the invention have been immobilized;

[0203] b) optionally, the reagents necessary to perform the hybridization reaction.

[0204] Additionally, the recombinant BAC vectors according to the invention and the polynucleotide inserts contained therein may be used for performing detection methods based on « molecular combing ». Said methods consist in methods for aligning

macromolecules, especially DNA and are applied to processes for detecting, for measuring intramolecular distance, for separating and/or for assaying a macromolecule, especially DNA in a sample.

[0205] These « molecular combing » methods are simple methods, where the triple line S/A/B (meniscus) resulting from the contact between a solvent A and the surface S and a medium B is caused to move on the said surface S, the said macromolecules (i.e. DNA) having a part, especially an end, anchored on the surface S, the other part, especially the other end, being in solution in the solvent A. These methods are particularly fully described in the PCT Application n° PCT/FR 95/00165 filed on February 11, 1994 (Bensimon et al.).

[0206] When performing the « molecular combing » method with the recombinant BAC vectors according to the inventions or their polynucleotide inserts, the latter may be immobilized (« anchored ») on a suitable substrate and aligned as described in the PCT Application n° PCT/FR 95/00165, the whole teachings of this PCT Application being hereby incorporated by reference. Then, polynucleotides to be tested, preferably under the form of radioactively or non radioactively labeled polynucleotides, that may consist of fragments of genomic DNA, cDNA etc. are brought into contact with the previously aligned polynucleotides according to the present invention and then their hybridization position on the aligned DNA molecules is determined using any suitable means including a microscope or a suitable camera device.

[0207] Thus, the present invention is also directed to a method for the detection of the presence of a polynucleotide of mycobacterial origin in a biological sample and/or for physical mapping of a polynucleotide on a genomic DNA, said method comprising:

[0208] a) aligning at least one polynucleotide contained in a recombinant BAC vector according to the invention on the surface of a substrate;

[0209] b) bringing into contact at least one polynucleotide to be tested with the substrate on which the at least one polynucleotide of step a) has been aligned;

[0210] c) detecting the presence and/or the location of the tested polynucleotide on the at least one aligned polynucleotide of step a).

[0211] The invention finally provides for a kit for performing the above method, comprising:

[0212] a) a substrate whose surface has at least one polynucleotide contained in a recombinant BAC vector according to the invention;

[0213] b) optionally, reagents necessary for labeling DNA;

[0214] c) optionally, reagents necessary for performing a hybridization reaction.

[0215] In conclusion, it may be underlined that the alliance of such BAC-based approaches such as described in the present specification to the advances in comparative genomics by the availability of an increased number of complete genomes, and the rapid increase of well-characterized gene products in the public databases, will allow the one skilled in the art an exhaustive analysis of the mycobacterial genome.

## **MATERIALS AND METHODS**

[0216] 1. DNA-preparation. Preparation of *M tuberculosis* H37Rv DNA in agarose plugs was conducted as previously described (Canard et al., 1989; Philipp et al., 1996b). Plugs were stored in 0.2 M EDTA at 4°C and washed 3 times in 0.1% Triton X-100 buffer prior to use.

[0217] 2. BAC vector preparation. pBeloBAC11 was kindly provided by Dr. Shizuya, Department of Biology, California Institute of Technology (Pasadena, CA). The preparation followed the description of Woo et al., 1994 (Woo et al., 1994).

[0218] 3. Partial digestion with *HindIII*. Partial digestion was carried out on plugs, each containing approximately 10 µg of high molecular weight DNA, after three one hour equilibration steps in 50 ml of *HindIII* 1X digestion buffer (Boehringer Mannheim, Mannheim, Germany) plus 0.1% Triton X-100. The buffer was then removed and replaced by 1ml/plug of ice-cold *HindIII* enzyme buffer containing 20 units of *HindIII* (Boehringer). After two hours incubation on ice, the plugs were transferred to a 37°C water bath for 30 minutes. Digestions were stopped by adding 500 µl of 50 mM EDTA (pH 8.0).

[0219] 4. Size selection. The partially digested DNA was subjected to contour-clamped homogenous electric field (CHEF) electrophoresis on a 1% agarose gel using a BioRad DR III apparatus (BioRad, Hercules, CA) in IX TAE buffer at 13°C, with a ramp from 3 to 15 seconds at 6 V/cm for 16 hours. Agarose slices from 25 to 75 kb, 75 to 120 kb and 120 to 180 kb were excised from the gel and stored in TE at 4°C.

[0220] 5. Ligation and transformation. Agarose-slices containing fractions from 25 to 75 kb, 75 to 120 kb and 120 to 180 kb were melted at 65°C for 10 minutes and digested with Gelase (Epicentre Technologies, Madison, WI), using 1 unit per 100 µl gel-slice. 25-100 ng of the size-selected DNA was then ligated to 10 ng of *HindIII* digested, dephosphorylated pBeloBAC11 in a 1:10 molar ratio using 10 units of T4 DNA ligase (New England Biolabs, Beverly, MA) at 16°C for 20 hours. Ligation mixtures were heated at 65°C for 15 minutes, then drop-dialysed against TE using Millipore VS 0.025

mM membranes (Millipore, Bedford, MA). Fresh electrocompetent *E. coli* DH10B cells (Sheng et al., 1995) were harvested from 200 ml of a mid-log ( $OD_{550}=0.5$ ) culture grown in SOB medium. Cells were washed three times in ice-cold water, and finally resuspended in ice-cold water to a cell density of  $10^{11}$  cells/ml ( $OD_{550}=150$ ). 1  $\mu$ l of the ligation-mix was used for electroporation of 30  $\mu$ l of electrocompetent DH10B *E. coli* using a Eurogentec Easyject Plus electroporator (Eurogentec, Seraing, Belgium), with settings of 2.5 kV, 25  $\mu$ F, and 99  $\Omega$ , in 2 mm wide electroporation cuvettes. After electroporation, cells were resuspended in 600  $\mu$ l of SOC medium, allowed to recover for 45 minutes at 37°C with gentle shaking, and then plated on LB agar containing 12.5  $\mu$ g/ml chloramphenicol (CM), 50  $\mu$ g/ml-X-gal, and 25  $\mu$ g/ml IPTG. The plates were incubated overnight and recombinants (white colonies) were picked manually to 96 well plates. Each clone was inoculated 3 times (2 X 200  $\mu$ l and 1 X 100  $\mu$ l of 2YT/12.5  $\mu$ g/ml CM per clone) and incubated overnight. One of the microtiter plates, containing 100  $\mu$ l culture per well, was maintained as a master plate at -80°C after 100 ml of 80% glycerol were added to each well, while minipreps (Sambrook et al., 1989) were prepared from the remaining two plates to check for the presence of inserts. Clones containing inserts were then designated "Rv" clones, repicked from the master plate to a second set of plates for storage of the library at -80°C.

[0221] 6. Preparation of DNA for sizing, direct sequencing and comparative genomics. A modified Birnboim and Doly protocol (Birnboim et al., 1979) was used for extraction of plasmid DNA for sequencing purposes. Each Rv clone was inoculated into a 50 ml Falcon polypropylene tube containing 40 ml of 2YT medium with 12.5  $\mu$ g/ml of CM and grown overnight at 37°C with shaking. Cells were harvested by centrifugation and stored at -20°C. The frozen pellet was resuspended in 4 ml of Solution A (50 mM glucose, 10 mM EDTA, 25 mM Tris, pH 8.0) and 4 ml of freshly prepared solution B (0.2 M NaOH 0.2% SDS) was then added. The solution was gently mixed and kept at room temperature for 5 minutes before adding 4 ml of ice-cold solution C (3M Sodium Acetate, pH 4.7). Tubes were kept on ice for 15 min, and centrifuged at 10,000 rpm for 15 min. After isopropanol precipitation, the DNA pellet was dissolved in 600  $\mu$ l RNase solution (15 mM Tris HCl pH 8.0, 10  $\mu$ g/ml RNase A). After 30 minutes at 37°C the DNA solution was extracted with chloroform:isoamylalcohol (24:1) and precipitated from the aqueous phase using isopropanol. The DNA pellet was then rinsed with 70% ethanol, air-dried and dissolved in 30  $\mu$ l distilled water. In general, DNA prepared by this method was clean and concentrated enough to give good quality results by automatic sequencing



(at least 300 bp of sequence). For a few DNA preparations, an additional polyethylene glycol (PEG) precipitation step was necessary, which was performed as follows. The 30  $\mu$ l of DNA solution were diluted to 64  $\mu$ l, mixed gently and precipitated using 16  $\mu$ l 4M NaCl and 80  $\mu$ l of 13% PEG 8000. After 30 min on ice the tubes were centrifuged at 4°C, the pellet carefully rinsed with 70% ethanol, air-dried and diluted in 20  $\mu$ l of distilled water.

[0222] 7. Sizing of inserts. Insert sizes were determined by pulsed-field gel electrophoresis (PFGE) after cleavage with *DraI* (Promega). 100-200 ng of DNA was *DraI*-cleaved in 20  $\mu$ l total reaction volume, following the manufacturer's recommendations, then loaded onto a 1% agarose gel and migrated using a pulse of 4 s for 15 h at 6.25 V/cm at 10°C on an LKB-Pharmacia CHEF apparatus. Mid-range and low-range PFGE markers (New England Biolabs) were used as size standards. Insert sizes were estimated after ethidium bromide staining of gels.

[0223] 8. Direct sequencing. For each sequencing reaction 7  $\mu$ l BAC DNA (300-500ng), 2  $\mu$ l primer (2  $\mu$ M), 8  $\mu$ l reaction mix of the *Taq* DyeDeoxy Terminator cycle sequencing kit (Applied Biosystems) and 3  $\mu$ l distilled water were used.

[0224] After 26 cycles (96°C for 30 sec; 56°C for 15 sec; 60°C for 4 min) in a thermocycler (MJ-research Inc., Watertown, MA) DNA was precipitated using 70  $\mu$ l of 70% ethanol/0.5 mM MgCl<sub>2</sub>, centrifuged, rinsed with 70% ethanol, dried and dissolved in 2  $\mu$ l of formamide/EDTA buffer. SP6 and T7 samples of 32 BAC clones were loaded onto 64 lane, 6% polyacrylamide gels and electrophoresis was performed on a Model 373A automatic DNA sequencer (Applied Biosystems) for 12 to 16 hours. The sequences of oligonucleotides used as primers are shown in Table 1.

[0225] 9. DOP-PCR. As an alternate procedure we used partially degenerate oligonucleotides in combination with vector-specific (SP6 or T7) primers to amplify insert ends of BAC clones, following a previously published protocol for P1 clones (Liu et al., 1995). The degenerate primers Deg2, Deg3, Deg4, Deg6 (Table 1) gave the best results for selected amplification of insert termini.

[0226] Table 1: Primers used for PCRs and sequencing

[0227] Vector specific Primers for DOP PCR- first amplification step:

[0228] SP6-BAC1: AGT TAG CTC ACT CAT TAG GCA (SEQ ID NO. 734)

[0229] T7-BAC1: GGA TGT GCT GCA AGG CGA TTA (SEQ ID NO. 735)

[0230] Vector specific Primers (direct sequencing, nested primer for second PCR step)

[0231] SP6 Mid: AAA CAG CTA TGA CCA TGA TTA CGC CAA (SEQ ID NO. 736)

[0232] T7-Belo2: TCC TCT AGA GTC GAC CTG CAG GCA (SEQ ID NO. 737)

[0233] Degenerate Primers:

[0234] Deg2: TCT AGA NNN NNN TCC GGC (SEQ ID NO. 738)

[0235] Deg3: TCT AGA NNN NNN GGG CCC (SEQ ID NO. 739)

[0236] Deg4: CGT TTA AAN NNN NWA GGC CG (SEQ ID NO. 740)

[0237] Deg6: GGT ACT AGT NNN NNW TCC GGC (SEQ ID NO. 741)

[0238] Primers used for the amplification of *M. bovis* DNA in polymorphic chromosomal region of Rv58:

[0239] Primer 1: ACG ACC TCA TAT TCC GAA TCC C (SEQ ID NO. 742)

[0240] Primer 2: GCA TCT GTT GAG TAC GCA CTT CC (SEQ ID NO. 743)

[0241] 10. Screening by pooled PCR. To identify particular clones in the library which could not be detected by random end-sequencing of the 400 BAC clones, PCR-screening of DNA pools was performed. Primers were designed for regions of the chromosome where no BAC coverage was apparent using cosmid-or H37Rv whole genome shotgun sequences. Primers were designed to amplify approximately 400-500 bp. Ninety-six-well plates containing 200 µl 2YT/12.5 µg/ml CM per well were inoculated with 5 µl of -80°C glycerol stock cultures each from the master plates and incubated overnight. The 96 clones of each plate were pooled by taking 20 µl of culture from each well and this procedure was repeated for 31 plates. Pooled cultures were centrifuged, the pellets were resuspended in sterile water, boiled for 5 minutes, centrifuged and the supernatants kept for PCRs. As an initial screening step, the 31 pools of a total of 2976 BACs, representing about two thirds of the library were tested for the presence of a specific clone using appropriate PCR primers. PCR was performed using 10 µl of supernatant, 5 µl of assay buffer (100 mM b-mercaptoethanol, 600 mM Tris HCl (pH 8.8), 20 mM MgCl<sub>2</sub>, 170 mM (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>), 5 µl of Dimethylsulfoxide (DMSO), 5 µl of dNTPs (20 mM), 5 µl of water, 10 µl primer (2 µM), 10 µl inverse primer (2 µM) and 0.2 units of *Taq* DNA polymerase (Boehringer). 32 cycles of PCR (95°C for 30 s, 55°C for 1 min 30 s, 72°C for 2 min) were performed after an initial denaturation at 95°C for 1 min. An extension step at 72°C for 5 min finished the PCR. If a pool of 96 clones yielded an appropriate PCR product (Fig. 1A), subpools were made to identify the specific clone. Subpools representative for lane A of a 96 well plate were made by

pooling clones 1 to 12 from lane A into a separate tube. Subpools for lanes B to H were made in the same way. In addition, subpools of each of the 12 rows (containing 8 clones each) were made, so that for one 96 well plate, 20 subpools were obtained. PCR with these 20 subpools identified the specific clone (Fig. 1B, lower gel portion). If more than one specific clone was present among the 96 clones of one plate (Fig. 1B, upper gel portion), additional PCR reactions had to be performed with the possible candidates (data not shown).

[0242] 11. Genomic comparisons. DNA from the BAC clone Rv58 was digested with the restriction endonucleases *Eco*R1 and *Pvu*II, and resolved by agarose gel electrophoresis at low voltage overnight (1.5 V/cm). DNA was transferred via the method of Southern to nitrocellulose membranes (Hybond C extra, Amersham) following standard protocols (Sambrook et al., 1989), then fixed to the membranes at 80°C for 2 hours. The blot was hybridized with <sup>32</sup>P labelled total genomic DNA from *M. tuberculosis* H37Rv, *M. bovis* type strain (ATCC 19210) or *M. bovis* BCG Pasteur. Hybridization was performed at 37°C overnight in 50% formamide hybridization buffer as previously described (Philipp et al., 1996b). Results were interpreted from the autoradiograms.

[0243] 12. Computer analysis. Sequence data from the automated sequencer ABI373A were transferred as binary data to a Digital Alpha 200 station or Sun SparcII station and analysed using TED, a sequence analysis program from the Staden software package (Dear et al., 1991). Proof-read sequences were compared using the BLAST programs (Altschul et al., 1990) to the *M. tuberculosis* H37Rv sequence databases of the Sanger Centre, containing the collected cosmid sequences (TB.dbs) and whole-genome shotgun reads (TB\_shotgun\_all.dbs) (<http://www.sanger.ac.uk/>). In addition, local databases containing 1520 cosmid end-sequences and the accumulating BAC end-sequences were used to determine the exact location of end-sequenced BACs on the physical and genetic map. MycDB (Bergh et al., 1994) and public databases (EMBL, Genbank) were also used to compare new sequences, but to a lesser extent. The organization of the open reading frames (ORFs) in the polymorphic region of clone Rv58 was determined using the DIANA software established at the Sanger Centre.

## EXAMPLES

[0244] Example 1 : Construction of a pBeloBAC11 library of *M. tuberculosis* H37Rv.

[0245] Partial *Hind*III fragments of H37Rv DNA in the size range of 25 to 180 kb were ligated into pBeloBAC11 and electroporated into strain *E. coli* DH10B. While cloning of fractions I (25 to 75 kb) and II (75 to 120 kb) gave approximately  $4 \times 10^4$  transformants (white colonies), cloning of fraction III (120 to 180 kb) repeatedly resulted in empty clones. Parallel cloning experiments using partial *Hind*III digests of human DNA resulted in stable inserts for all three fractions (data not shown), suggesting that the maximum size of large inserts in BAC clones is strongly dependent on the source of the DNA. Analysis of the clones for the presence of inserts revealed that 70% of the clones had an insert of the appropriate size while the remaining 30% of white colonies represented empty or *lacZ'*-mutated clones. Size determination of randomly selected, *Dra*Icleaved BACs via PFGE showed that the insert sizes ranged for the majority of the clones between 40 kb and 100 kb with an average size of 70 kb. Clones with inserts of appropriate size were designated with "Rv" numbers, recultured and stored at -80°C for further use.

[0246] Example 2 : Direct DNA sequence analysis of BACs.

[0247] To characterize the BAC clones, they were systematically subjected to insert termini sequencing. Two approaches, direct sequencing of BAC DNA and PCR with degenerate oligonucleotide primers (DOP), adapted to the high G+C content of mycobacterial DNA, were used. In a first screening phase, 50 BAC clones designated Rv1 to Rv50 were analysed using both methods in parallel. Except for two clones, where the sequences diverged significantly, the sequences obtained by the two methods only differed in length. Sequences obtained directly were on average about 350 bp long and for 95% of the clones both the SP6 and T7 end-sequences were obtained at the first attempt. Sequences obtained by DOP-PCR were mostly shorter than 300 bp. For 40% of the BACs we obtained only very short amplicons of 50 to 100 base pairs from one end. In two cases the sequence obtained with the DOP-PCR differed from the sequences obtained by direct sequencing, and in these cases *E. coli* or vector sequences were amplified (data not shown). Taking the advantages and disadvantages of both methods into account, we decided to use direct termini sequencing for the systematic determination of the SP6 and T7 end-sequences.

[0248] Example 3 : Representativity of the library.

[0249] After having determined the end-sequences of 400 BACs a certain redundancy was seen. The majority of clones were represented at least 3 to 4 times. Maximum redundancy was seen in the vicinity of the unique *rrn* operon, as 2.5% of the

clones carried identical fragments that bridge the cosmids Y50 and Y130 (Fig. 3, approximate position at 1440 kb). The majority of clones with identical inserts appeared as two variants, corresponding to both possible orientations of the *Hind*III fragment in pBeloBACII. This suggests that the redundancy was not the result of amplification during library construction, but due to the limited number of possible combinations of partial *Hind*III fragments in the given size-range of 25 to 120 kb. To detect rare BAC clones, a pooled PCR protocol was used. Primers were designed on the basis of the existing cosmid sequences and used to screen 31 pools of 96 BAC clones. When positive PCR products of the correct size were obtained, smaller subpools (of 8 or 12 clones each) of the corresponding pool were subsequently used to identify the corresponding clone (Figs. 1A and 1B). With this approach 20 additional BACs (Rv401-Rv420) were found for the regions where no BACs were found with the initial systematic sequencing approach. The end-sequences of these BACs (Rv401-420) were determined by direct sequencing, which confirmed the predicted location of the clones on the chromosome. A 97% coverage of the genome of H37Rv with BAC clones was obtained. Only one region of ~ 150 kb was apparently not represented in the BAC library as screening of all pools with several sets of specific primers did not reveal the corresponding clone. This was probably due to the fact that *Hind*III fragments of mycobacterial DNA larger than 110 kb are very difficult to establish in *E. coli* and that a *Hind*III fragment of ~ 120 kb is present in this region of the chromosome (data not shown).

[0250] Example 4: Establishing a BAC map.

[0251] Using all end-sequence and shotgun-sequence data from the H37Rv genome sequencing project, most of the BAC clones could then be localized by sequence comparison on the integrated map of the chromosome of *M. tuberculosis* strain H37Rv (Philipp et al., 1996b) and an ordered physical map of the BAC-clones was established. PCR with primers from the termini sequences of selected BACs were used for chromosomal walking and confirmation of overlapping BACs (data not shown). The correct order of BACs on the map was also confirmed more recently, using 40,000 whole genome shotgun reads established at the Sanger Centre. In addition, pulsed-field gel electrophoresis of *Dra*I digests of selected BACs was performed (Fig. 2) in order to see if the approximate fragment size and the presence or absence of *Dra*I cleavage sites in the insert were consistent with the location of the BACs on the physical map (Fig. 3). Comparison of the sequence-based BAC-map with the physical and genetic map, established by PFGE and hybridization experiments (Philipp et al., 1996b), showed that

the two maps were in good agreement. The positions of 8 genetic markers previously shown on the physical and genetic map were directly confirmed by BAC-end-sequence data (Table 2, Fig. 3). The position of 43 from 47 Y-clones (91%) shown on the physical and genetic map, which were later shotgun sequenced, was confirmed by the BAC end-sequences and shotgun sequence data. Four clones (Y63, Y180, Y251, and Y253) were located to different positions than previously thought and this was found to be due to book keeping errors or to chimeric inserts. Their present approximate location relative to the *oriC* is shown in Figure 3: Y63 at 380 kb, Y63A at 2300 kb, Y180 at 2160 kb, Y251 at 100 kb, and Y253 at 2700 kb. A total of 48 BACs, covering regions of the chromosome, not represented by cosmids were then shotgun sequenced (Cole et al., 1997), and these are squared in Fig. 3. No chimeric BACs were found, which is consistent with the observations of other research groups for other BAC libraries (Cai et al., 1995; Zimmer et al., 1997). The absence of chimeric BACs was of particular importance for the correct assembly of the *M. tuberculosis* H37Rv sequence. The exact position of the BAC termini sequences on the chromosome will be available via the world wide web (<http://www.pasteur.fr/MycDB>).

[0252] Table 2 : Identities of genetic markers previously shown on the integrated and genetic map of H37Rv. (Phlipp et al., 1996b) which showed perfect sequence homology with BAC end sequences.

Locus	BAC end sequence	Description of genetic marker	Organism	GenBank Accession n°
<i>apa</i>	Rv163SP6	Secreted alanine-proline-rich antigen	<i>M. tuberculosis</i>	X80268
<i>dnaJ, dnaK</i>	Rv164T7		<i>M. leprae</i>	M95576
<i>fop-A</i>	Rv136T7	DnaJ hsp	<i>M. tuberculosis</i>	M27016
<i>polA</i>	Rv401T7	Fibronectin binding protein	<i>M. tuberculosis</i>	L11920
<i>ponA</i>	Rv273T7		<i>M. leprae</i>	S82044
<i>pstC</i>	Rv103T7	DNA polymerase I	<i>M. tuberculosis</i>	Z48057
<i>recA</i>	Rv415SP6	Penicillin binding protein	<i>M. tuberculosis</i>	X58485
<i>wag9</i>	Rv35SP6	Putative phosphate transport receptor	<i>M. tuberculosis</i>	M69187
		Homologous recombination 35-kDa antigen		

[0253] Example 5 : Repetitive end-sequences.

[0254] Repetitive sequences can seriously confound mapping and sequence assembly. In the case of the BAC end-sequences, no particular problems with repetitive sequences were observed. Although nine clones with one end in an *IS1081* (Collins et al., 1991) sequence were identified, it was possible to correctly locate their position on the map using the sequence of the second terminus. Moreover, these BACs were used to determine the exact locations of *IS1081* sequences on the map. Five copies of this insertion sequence, which harbors a *HindIII* cleavage site, were mapped on the previous physical and genetic map. In contrast, BAC end-sequence data revealed an additional copy of *IS1081* on the *M. tuberculosis* H37Rv chromosome. The additional copy was identified by six clones (Rv27, Rv118, Rv142, Rv160, Rv190, Rv371) which harbored an identical fragment linking Y50 to I364 (Fig. 3, at ~ 1380 kb). This copy of *IS1081* was not found by previous hybridization experiments probably because it is located near another copy of *IS1081*, localized on the same *DraI* fragment Z7 and *AsnI* fragment U (Fig. 3, at ~ 1140 kb). Furthermore, the position of a copy of *IS1081* previously shown in *DraI* fragment Y1 (Fig. 3, at ~1840 kb) had to be changed to the region of Y349 (Fig. 3, at ~ 3340 kb) according to the end-sequences of BAC Rv223. The positions of the four other *IS1081* copies were confirmed by the sequence data and therefore remained unchanged. In total 6 copies of *IS1081* were identified in the H37Rv genome in agreement with the findings of others (Collins et al., 1991).

[0255] In addition, a sequence of 1165 bp in length containing a *HindIII* site was found in two copies in the genome of H37Rv in different regions. The end-sequences of BAC clones Rv48 and Rv374, covering cosmid Y164, as well as Rv419 and Rv45, that cover cosmid Y92, had perfect identity with the corresponding parts of this 1165 bp sequence (Fig. 3, at ~ 3480 kb and ~ 900 kb). Analysis of the sequence did not reveal any homology with insertion sequences or other repetitive elements. However, as each of the two locations showed appropriate BAC coverage, chimerism of the sequenced cosmids Y164 and Y92 can be ruled out as the probable cause.

[0256] Example 6 : Using BAC clones in comparative genomics.

[0257] The minimal overlapping set of BAC clones represents a powerful tool for comparative genomics. For example, with each BAC clone containing on average an insert of 70 kb, it should be possible to cover a 1Mb section of the chromosome with 15 BAC clones. Restriction digests of overlapping clones can then be blotted to membranes, and probed with radiolabelled total genomic DNA from, for example, *M. bovis* BCG Pasteur. Restriction fragments that fail to hybridize with the *M. bovis* BCG Pasteur DNA

must be absent from its genome, hence identifying polymorphic regions between *M. bovis* BCG Pasteur and *M. tuberculosis* H37Rv. The results of such an analysis with clone Rv58 (Fig. 3, at ~ 1680 kb) are shown here. This clone covers a previously described polymorphic genomic region between *M. tuberculosis* and *M. bovis* BCG strains (Philipp et al., 1996a). *EcoRI* and *PvuII* digests from clone Rv58, fixed on nitrocellulose membranes, were hybridized with <sup>32</sup>P-labelled total genomic DNA from *M. tuberculosis* H37Rv, *M. bovis* (ATCC 19120), and *M. bovis* BCG Pasteur. Figures 4A and 4B present the results of this analysis, where it is clear that several restriction fragments from clone Rv58 failed to hybridize with genomic DNA from either *M. bovis* or *M. bovis* BCG Pasteur. On the basis of the various missing restriction fragments, a restriction map of the polymorphic region was established and compared to the H37Rv sequence data. The localization of the polymorphism could therefore be estimated, and appropriate oligonucleotide primers (Table 1) were selected for the amplification and sequencing of the corresponding region in *M. bovis*. The alignment of *M. bovis* and *M. tuberculosis* H37Rv sequences showed that 12,732 bp were absent from the chromosomal region of the *M. bovis* type strain and *M. bovis* BCG Pasteur strain. The G+C content of the polymorphic region is 62.3 mol%, which is the same as the average genome G+C content of the *M. tuberculosis* genome, hence indicating that this region is not a prophage or other such insertion. Subsequent PCR studies revealed that this segment was also absent from the Danish, Russian, and Glaxo substrains of *M. bovis* BCG, suggesting that this polymorphism can be used to distinguish *M. bovis* from *M. tuberculosis*. Analysis of this sequence showed that 11 putative open reading frames (ORFs) are present in *M. tuberculosis*, corresponding to ORFs MTCY277.28 to MTCY277.38 / accession number Z79701 -EMBL Nucleotide Sequence Data Library (Fig. 5). FASTA searches against the protein and nucleic acid databases revealed that the genes of this region may be involved in polysaccharide biosynthesis. Among these putative genes, the highest score was seen with ORF 6 (MTCY277.33), whose putative product shows a 51.9% identity with GDP-D-Mannose dehydratase from *Pseudomonas aeruginosa* (accession number U18320 - EMBL Nucleotide Sequence Data Library) in a 320 amino acid overlap. The novel *M. bovis* sequence of the polymorphic region was deposited under accession number AJ003103 in the EMBL Nucleotide Sequence Data Library.

[0258] As it appears from the teachings of the specification, the invention is not limited in scope to one or several of the above detailed embodiments; the present invention also embraces all the alternatives that can be performed by one skilled in the same technical field, without deviating from the subject or from the scope of the instant invention.



**Table 3 : End-sequences of the polynucleotide inserts cloned in the named recombinant BAC vectors contained in the 1-1945 *M. tuberculosis* H37Rv genomic DNA library.**

RvXXXSP6 corresponds to the SP6 end-sequence of the clone RvXXX.

RvXXXT7 corresponds to the T7 end-sequence of the clone RvXXX.

RvXXXIS 1081 corresponds to a region located close to a copy of the IS1081 repetitive sequence (Insertion element).

The character « - » denotes an uncertain base residue.

**Clone Rv101**

.....Rv101SP6.seq:.....

AATACTCAAGCTTGCCCGAGCCGTCGATGACAAGAAATATGTCCGCAAAAGACTCAGCGGCCGACTTTGCTCGCAGCTG  
GCGGTACCGCGCCACCGATTCTATGCCGTGGTCGCGGAAAAATGCCTCCCGAAATCGCACGGCCGACTCCAGTTTCGGC  
GAGCATCCGCGATGCCAGCTGCGGCTGCGCCCTGCCGGCCACGGCACCCACATGCGGCAGTTCGTCCACCTGGGCCAG  
CGCCCCGCGCCGAATTCCAAACAATAGAACTGCACCCGGCCCGCATCGTGGGTAAACAGCCAACGCCATGATCAGCGT  
CCGCGAGCGCGGTTGACTTGCCCGTTTTCGGGTGCACCTACGAACGCGACATTGCCTGCGGCCCCGGACAAGTCGATCGT  
GCGCGGCACCCGTGACTGCTCTAACGGGCGATTGAAATCCGAT (SEQ ID NO. 6)

.....Rv101T7.seq:.....

CCACCCGTGTAATTTGGGATGGGCAAAAAGGCGAAGCACCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGG  
TTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCAACACCTCGCGTCGCCCTCCGACCGCGAACATTTCGGGG  
ATGGCAGCAACCTGCTGGCACCCCTGGCCGGGCGATGATCTGCAGCGTCGCCCGGGTAGTCGCCGCCCGGGCGGCTAC  
ACTCTGAAACGCGATGACCATCGATGTGTGGATGCAGCATCCCGACGCAACGGTTCCTACACCGCGATATGTTTCGCT  
CGCTGCCCGGTGGACCGGT (SEQ ID NO. 7)

**Clone Rv102**

.....Rv102SP6.seq:.....

AATACTCAAGCTTTCCGCGGATACCCGCCATGTCGCGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGCGGG  
ATCCCAAAGTGCGGATGATCGGGCCGCTACGTCTGTGGTGTACCTCGTCGGTAACAACGAAACCGAAGCGTATGACTC  
GGTCCACGCGGTGCGGCACATGGTGGACACCACCGCCACCGGCGGGGTGAAGGCCTATGTACCCGGTCCGGCAGC  
ACTCAATGCCGACCGAGGCGGAGGACAAAAGTATCGCTAAGGTACCGCGATCACCAACATGGTGATCGCAGC  
AATGTTGCTAGTGATCTATCGCTCCGTAATTACCGCGGTTCT (SEQ ID NO. 8)

.....Rv102T7.seq:.....

GTGCCGTTCCAACCCGAATTGGCTTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCTGTCGC  
GGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGC  
TTCCGCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCGGAGCG  
ACGGCCAAGGCGGCGTGCCAGGTGCCCCGGGCGCACGGTGCGGACAAGGTGGTGTGGCGGTCCCGATCGGCCAGAC  
GACATCGTGGCGAGATTCGCCGGGTACGCCGATGAGGTGGT (SEQ ID NO. 9)

**Clone Rv103**

.....Rv103SP6.seq:.....

AATACTCAAGCTTTCCGCGGAAACGGACACATTGCGAATATTGATGACAAAATAAAAATCATTGATGGTTTGAGTCAC  
CAGGCCGATCAAGCCTTCGCCGAGCCAAATTCCAATCAAGAGGCCCAAGCCGTACCAATCAGCCCCGGCAACGAGGGA  
TTCCGTCATTATCAGCCAAAATAACTGCTCTCGGGTTACACCCAAACAGCGCAATATGGCGAAAAACGGTCGCCGTTG  
CAGGACATTAAATGTCACGGTATTGTAGATTAAAAAGATACCCAC (SEQ ID NO. 10)

.....Rv103T7.seq:.....

TGCTCCCGAAACCTGGGGGTGTGCCTGCTCTGTATGCACGGCATAACGGACATCCTTCCCCTGAGACCCGCGGTGCAAC  
CAGCCACGTGTCCATCATAGNGGTCAACCCCGGCCAAGGGCGACGGCACGCCAAGTTCGCCGACCGTTAACCTAGTG  
CTGTTAGCTTCATTGCTGCGATCAAAACAGCTGGTCGGCCGTAGGAACTGAATTGAACTCAACCGATTGTTGGTGCC  
GCCGTAGGTGTCTGGCTGCGGGTGCGCTGGTGTTCGCGGTGTGTTAACGACGACAATGTGACCGGGGGAGGTGCA  
ACCACTGGCCAGGCGTCGGCAAAGGTCGATTGCGGGGGGAAGAAGACACTCAAAGCCAGTGGGT (SEQ ID NO. 11)

## Clone Rv104

.....Rv104SP6.seq:.....  
ATACTCAAGCTTTGCCGACGAGCGGGCGATGTTGATGACGGGAAACCCAGCGCACAACCGACGATTTTGGCGTAGCC  
GGCGGACGCTCTGCTCGATTCCGATCACGTCGGCGCTCGCATCGAGCATGGCGCGCGGCGACGGCTAGCAGCGATCCGCC  
GTCGTCGAGGAGCACGACACGAGCCGTACGCCGGCCGTAAGCCGCGCCAGGATTCGGCGAAAAACCGTTCTACGTG  
GCGGGTGTACTGGGTGTGAATGATTCTGTTGGGTGCGTAGGCGTCGCTGCAATCGTCGACATAGATGCCGTGGGGCCG  
CATCGCGTCGACAACCTCCGGGTGAGTGGAATAGCACTTGCCGATCACCGCGACGTTGCGCGGATGAGGCCGAACCCGA  
ATA (SEQ ID NO. 12)

.....Rv104T7.seq:.....  
TCCTATGTCCCTGCCGAGCANGTGATCGAACGCGGTGACAGATTTGTCTATCCTGGACCTGACGGTGAGGTGGAAGTT  
TTCCAGGAATTCCGCAAAATCGGTAAGAGCCTGAAGAATTCTGGTATCGCCGGACGAAATCTGCGACGCATACGGGGGC  
ATATACGCTTCGGGTTTACGAGATGTCGATGGGGCCGCTGGAGGCTTACGTCCATGGGCCACAAAGGATGTTGTCTCG  
CGCGTACCGTTTCTGCAGCGGGTGTGGCGCTTGCTCG (SEQ ID NO. 13)

## Clone Rv105

.....Rv105SP6.seq:.....  
ATACTCAAGCTTGATTCCGCCGAAACCGACCGTGAGCACCCTGCCAGCCACCACGCTCGGGTCGGGCGCGGGCCCGG  
GCCGCCAGGCTGCTCCGCTCGGTGATGGCAGCCACCCTGCCAGCACCACCGGCTGCGTACGTCTAACCATTCCAGGCG  
GAGCTACATCAGCTCGGCCGCCAGTGTTCGGGCCCTCTTTCCAGGTCGAAGTCTATACCGATATGCGCATCCGCAGC  
CGCCACCCTGGAGAACAGACGATGCCCTACTAATGCTTGTCTGGCGGGGCC (SEQ ID NO. 14)

.....Rv105T7.seq:.....  
GGTACGCTTCGGTCGCAGTCTGCGAGTGATGCATGACGACCGGGACCTCGTCGGCATCTTCCATAGCCCCGCCACACCT  
TCAGTTGCTCACCGGAATCCAACCGGTAGAAGGTCGGCGAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCGGGAC  
GGTCAGAGCCCTCGGGTCCGGCCAGCACTCCGCAGGCTTCGTCGGGGTGGTCGCGACGCGCATGGGCCACCATCGCAT  
TCACCAGGTCTGCGCGAATCACGACGACGTAGACGGTTCTTTCTTAAGCAACACCGGAAGTTTCAGGACCGGAATGCT  
CCGGGAAACATGTCACGGTAGGTGCGGTATTCCGGCTACCGGCTGA (SEQ ID NO. 15)

## Clone Rv106

.....Rv106SP6.seq:.....  
GGCGTCAACGGTGTCGGAACCCGCGTCAAGCAATTGGTAGGCCTGCAGTCTGTGAATCAGGCCGACGCTGTGGCCGCC  
GCGGC (SEQ ID NO. 16)

.....Rv106T7.seq:.....  
GGCTNGCGTACCCGGTACCGGCCGCGGGCCTACCAGTGCCGGAAGTGAAGCGCAGTAAGCCCTCAACGCGCCACCG  
CTTTGGCCGCGCGCCCCGGCGTAGGCGCATCGGCGGTGGCCGTGGGGCGGCGCACTGCGACCTCACCAGCGGCTTTCCG  
AGCTTTGTTTCGATCAACCGGCCAGCATGGTTCGANGATGCATTTCGAGACCATATTCGAAATTGGTTTCATCGGGGGCCC  
CGATCCGATGCCCCCTCCAGTTGCGTGAGCAANCAGCGAGTCNTCGCGGGATCGATGGCCACGGGGTGTTCATGG  
CGGATGGTCCGCTGCCCGCCGACTGGCTCTTGCGGGGAGAACCAGTCTAGCACCACCGATCCGCGCACGTNG  
(SEQ ID NO. 17)

## Clone Rv107

.....Rv107T7D4.seq:.....  
CGTAATNTCGCGCACANCCANGACTTCTGGGGGGATCNGCTGACAGTGGTNGGATCCCAAATTGCGGATGATCGGGCC  
GCCNACGTCGTTGTGTACCTCNCNTGTCACAACNAANCCGAANCATGACTCGGTCCACGCGGTGCGGCACATGGTG  
GACACCACACCGCCACCGCNCGGGGTGAAGGCCTATGTCACCGGTCCGGCAACACTCAATGCCGACCAGGCCGANGCC  
GGACACNANAGTATCNCCTAACGTACCGCGATCACGAGCATGGTGATCGNNCAATGTTNCTANTGATCTATCGCTCCG  
TAATTACCGCGGTTCTCGTCTTGATCATGGTCGCANCGAACTCCGGCGCAATCCGCGGATTCATCGNCTTGGTCCGCCG  
ATCACATATTTTCAGCCTTTCACATTGCAACNAACCTGCTCGTCTCATGGNGATGCGGCGACACGGACTACCGATATC  
ATGCTCGCCGTTACACAATCNCGCCACGCCGCGAAGACNGGAACGTTCTACACAATNTTNCGGGACGCCACTNAA  
CTTGGTTCNGGTTTGACATTGCCGCGCATGNTGCCAGCTTTGCCGGCTCCCCTTA (SEQ ID NO. 18)

## Clone Rv108

.....Rv108T7D4.seq:.....  
TGAATTTCCCGATCCCAATCTCGGTTTCAGATACAGGTGCGCATACCCCTTACTTCGGCAACGCTGGGCGGATTGGC  
CCTGCNGCTGCAGCANACCATCGACGCCATCGAATTGCCGGCAATCTCGTTCAGCCAATCCATACCCATCGACATTCC  
GCCGATCGACATCCGGCCCTTCNCCCTTAACGG (SEQ ID NO. 19)

## Clone Rv109

.....Rv109SP6.seq.....  
AACAGCTATGACCATGNTTACGCCAAGCTATTTAGGTAACACTATANAATACTCAAGCTTTTACGGTGATCGCGCATC  
ACCTGGTTTCATGAACTGGAAGCAGCGCANCCTTCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCCGCGGTTCNGG  
TGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAACCAGCTTCCATATCCCGCGACNAACNACNCC  
AGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTTCTCCACCGACCGGGCCGGGTGTGGGGTGT  
TTCCGGCGACCGCGAGCCAGGTGGTCCACACTGCCGACGGGCGCCGCGAGCCGTTACCCGACCAAGCCGCGCAACAAGT  
CCGCCCAGATCGCATACTCCAACCGGTTGCGGTACTGCAGGTGAGCTGGCGTACCTCCTCNTCNCGCTCGGCGAAGTCT  
TGCTCCANACAGTCGCGAGAACGGCAAGGAACACGTTCA (SEQ ID NO. 20)

.....Rv109T7.seq.....  
GACCGNNCCATGTTTCCACAATGTGGTGCCAGTNCGGNGGCTACGTGCCATCNANAACTGGCGCAGGCTATCGCACC  
CGTTATCNGCTACGAACAAATCNCGGTATGCGTCTTTTANCATGAGTCGGCGACCGNCGATCATGGTCGACACCCACG  
ACNGAAATACGCGATCGCNCNTCAGCNCNTGTGTCCCGCGGATTATCANGACTGACCTCCTGGCTGACCGGNNTGTNTG  
GTCCGCGATGCCTGGCGCCCGCGCGGTGNTCGTGGTCCGCTCGGATAGCGAAGTCAGCTAATTCTCGTGGCAGCTCG  
AAAGGGTCTTCCGGTGCCGGTCTTTGCGCAAACCATGCNCATGTTACGGTCCCTCGGGTCCGGCCTGGCGGGCGGC  
(SEQ ID NO. 21)

## Clone Rv10

.....Rv10SP6D2.seq.....  
GGGATGGGCGGGCCCGCTAAACTCTTCGTGTCCACTAACTCCGGGAGGGNCAATCTCGGGCCGTTATGGCTCACGTC  
GCGTCGCCCTCCGACCGCGAACATTCCGAGTTGGCAGCAACCTGGTAGCACCTGGCCGG (SEQ ID NO. 22)

.....Rv10T7D4.seq.....  
NCCGTGTTGACAAGTAAATATGTCCGCAAAGTCTCAGCGGCCGACTTTGCTCGCAGGTGGCGGTACCGCGCCACCG  
AGTCGATGCCGTGGTTCGCGGAAGAATGCCTCCCGAAATCGCACGGCCTTCCCNNTTTAAACGGA (SEQ ID NO. 23)

## Clone Rv110

.....Rv110SP6.seq.....  
TTTAGGTGACACTATAGAATACTCAAGCTTTTGGTCTAGCCGGCCGAGCAGGATACGGGTGTCTATTGGCCACCGGCGG  
CGGCTGTCCGGGAAATGGCGGGTCCCCGGTGGTTTGTCTGATGAGTGCTGAACCGTANTCGAAGTGGGCGGGCTCAGA  
CTCCACCCANCCAGCAGGCGCGGAAGCTGAATCCTCCAACCGGGTGTGTCNATCCGGACAAGTTGGGGTGCCTTTGG  
GGCAATGACAGGTGGCNGCGGTGCGTTCGGGTCCGCCGGCGGAAGTGCTGCGTTGGGATCNCCTGGGTGGGCATTTCGGC  
NTTTTTCGGCGGGCGGTGGTNGGGGGGCAACAGGTNTCCCNCTGCGGGTGGCGCTCAACGGTCNACGGCGCAAGCCG  
CCGTTGTTGGTACCNGGGGCGCTGGCTCCGATCGCGTTGGCGGTNCNCCG (SEQ ID NO. 24)

.....Rv110T7.seq.....  
CTACACCATCGAATACGACGGCGTCGCCNACTTTCCGCGGTACCCGCTCAACTTTGTGTGCGACCCTCAACGCCATTGC  
CGGCACCTACTACGTGCACTCCAATACTTTCATCCTGACGCCGGAACAAATTGACGCGAGCGGTTCCGCTGACCAATAC  
GGTCGGTCCCAGATGACCCAGTACTACATATTTCGCACGGANAACCTGCCGCTGTAGAGCCACTGCGATCGGTGCC  
GATCGTGGGGAACCACTGGCGAACCTGGTTCAACCAAACTTGAANGTGATTGTTAACCTGGGCTACNGCGACCCGGC  
CTATGGTTATTTCNACCTCNCGCCCAATGTTGCGACTCCGTTCCGGTTGTTCCCANAAAGTCNNCCGGTCTGTCATCGC  
CGAANTCTCNTCCCGGGACCCACAGGGAATCNGCNATTTTCNCCTACAAATCANCCACCTCCA (SEQ ID NO. 25)

## Clone Rv111

.....Rv111T7.seq.....  
GCATGATCGGCCACCTTTTCGGGCCGCCCGGCATACGGCGGCGTACCGATCTCCGCGTCATACACCCGCGGGTAATCGC  
CGACGGTGCCGGTTCGCGAGCCGAAGGTGACGACTCTGATTGAATCGAGTTCAGGTCCAGCGGGTGGCGCACCAACG  
GCGCGAGCTAACGACGTCAATCNCGTTGTCGCTTTCTACGGTCACCGACCCTGGTGACCGTAGTTTCNCCCG  
(SEQ ID NO. 26)

## Clone Rv112

.....Rv112SP6.seq.....  
GACACTATAGAATACTCAAGCTTGCCAACCGCCAGCCTGCATCCGGCGGCGANCACTGCTCCGCCGACCAAGTACGAAC  
CAACCTGCGGTGCCCAGGCCATTGACGATGTGCTGGTCCGGCGCCCGGAGTCCGCGCACCATCAACGCCGCGGGCACC  
ACCANGGCGGCCCCACCCTGCACGGCGACGATCATTCGGCGCCGCTCACGGCGGGCGGGCTCGAACANGCACAGCA  
TCAACGTNGTCACCCGGCCGTGACCGGCCCGCATCGTCACACCACCAAGCCATTGCGGTCTCTCTCAACNGGGCGA  
CCCGGCCCGCATCGTCACACGGNCTAAGGCCATTGCCGTCTCTCT (SEQ ID NO. 27)

.....Rv112T7.seq.....

TCGGCGCCATCGGCACCTTCGAGGACCTGTATTTTCGACGCCGTGGCCNACCTGAGGTTGGCGGTGGACNAAGTGTGCA  
CCCCGTTGATTCGCTCGGCCTTGCCGGATGCCACCCNGCGCTGGTGGTCGATCCGCNAANAGACAANTTGTGGTGA  
NGCTTCTGCTGCTGCGACACCCACNACGTGGTGGCACCAGGCGAGCTTTAGCTGGCATGTCTGACCGCGCTGGCCGA  
CNACTCCAGACNTTCCACNAANGGTCGCCNNCCCAATGTNCCGNANTGTCTCCGGNTCCCTTTACCNCCCCAATGGGCN  
GNTTCCACNGGTTACGGGCCCCNTNCCGGCGGGTCTNCTCCCAANCTACCAAATACGCCCGACNTTCCGGA

(SEQ ID NO. 28)

## Clone Rv113

:Rv113SP6.seq:::

ATACTCAAGCTTTTATGGTGATCGCGCATCACCTGGTTCATGAAGTGAAGCAGCGCAGCGCTTCTTTTCGGCCGCA  
ACATGAGCCAGCTCTCGTCGGCGGTTCGGGTGCAGGTGCTCGGGCAGCTCGGCCGCGAACAGCCCGGCTTGAACCTG  
AAAACNGCTTTCCATATCCCGCGACGAAAGAACGCCAGTTCGGCTACTTAACCCCTCCGCGAACCGTCCATGGACAA  
CAGCGCGTTCCTCCACCAACCGGGCCCCGGGTGT (SEQ ID NO. 29)

:Rv113T7.seq:::

TCGGCTCAGGCCGCGCTGCTGGTAGAGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTCGGCGGCTACGT  
GCCATCGAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTACGAAGCAAATCGCGGTATGCGTTCTTGAGCATGA  
GTCGGCGACCGTCTCATGGTCGACACCCACGACGGAAGACGCGATCGCCGTCAGCATGTGTGCCCGGGATTATC  
AGGACTGACCTCCTGGCTGACCGGCATGTTTGGTCGCGATGCCTGGCGCCCGGGCGCGGTGGTGGTGGTGGTGGTGGT  
TAGCGAGGTCAGCGAATTCTCGTGGCAGCTCGAAAGGTCCTGCCGGTGCCGGTCTTTGCGCAACAATAGCGCAGGT  
TACGGTCGCGCGGGGTGCGGCCTGGCGGCGGCC (SEQ ID NO. 30)

## Clone Rv114

:Rv114SP6.seq:::

CAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCGCGTCTACGCCGGCCCCGAGCATCCGCACAGCGCTCAGCA  
GCCGGTTCGGTACGANCTCAAGCAGGTGGCGCAATGACCGAAACCACCCAGCCCCGCAAAACCCCGGCGGCCCGGCC  
GGGCCCCGACAATCGTTCGTGTTGGAGCGGCCCATCCANACCGTTGGGCGCCGTAAGGANGCCGTGGTACGAATGCGG  
CTGGTGCCCGGCACCGGCAAGTTCGACCTCAACGGCCGAGCTTGGANGACTACTTCCCAAACAAGGTGCACCAGCAG  
TTGATCAAGGCACCCCTGGTCACCGTGGATCGGGTGGAAAGTTTCGACATCTTTGCCACCTGGGCGGCGGCGGCCGT  
CCGGTCAGGCCGGGCTGCCCTGGGTATCGCCCGGCATTGATTCTGGTATCCCNAGAAGACCG (SEQ ID NO. 31)

:Rv114T7.seq:::

CGGTTGGCCACCGCTTCTGCGGTGCGCGCGCGCTCGACAATGACCGTGTCTGCTTCTGCTGACCACCACGCGTCGGGCC  
GAGCCAGCACCTCCAAGCCACCTCGCGCAGCACCATGCGCGCGTTCGGGGTTGACCACCTGGCCACCCGTACCCACC  
GCCAGGTCTCAAGGAAACGCCTTACGGCGGTACCGAAGTACGGCCCTTGACCGCGACCGCTTTCAACGTCTTGCG  
AATCGCGTTGACGACCAGCGTCGCCAACGCTTCGCCCCACAGTCTTCAGCCACGATCAGTAGTGGCTTACCCGTTCC  
TGCAACCTTTTCAGCAATGGCAACAGATCGGGAAGCGANCTGATCTTGTCTTGGTGCN (SEQ ID NO. 32)

## Clone Rv115

:Rv115SP6.seq:::

CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTTTGGTGGGTGCGCTTCGAATTCNGCGTGCACCGCTATGG  
GTTGCANAGCGGTGGCGCCGACACCCCACTGGCCCGGGTGTTCGCCCCGAACCCGGATCATGGTGAGCGAAAA  
GGANATTCNCCTGTTGATGCTGGGATTCGCCACGCCAAGGCATCTANCGATTACTCTCCNCGGGGTGGGAAAAGTGC  
CCAATCCCCCTCCCTCAACTTTCCNAACAATCATTCGGTTCNCNCTCCGGTTGGNGGTAACCNCCAATAAAACC  
CCTGCCCG (SEQ ID NO. 33)

:Rv115T7.seq:::

GCCCGCNCATGGCAATCCCCGAAGACATCATTGGCCAGTGGCCGGGCGCTAACAGGTTCCAGCCCCCACCANTGCC  
GCTCGAATGCGGTGCAACCCATTTCGAGGCCGCGAGGAAAGCACCAGCGGAAGCCGCAAGGGGTGCAGTTCGCG  
CCCAATAATGTCGTCCGCAACAGATGCGCTCNAAAACCNCCGGCAGTCAGCGCACCCGACGCGANGTCGAAAGAC  
GTCNTCAGCGCGCCACATGGGGTGCCAATCGGCACGGCAGGTATGCCGCGCGCAACCCGAGCGCGTGGTGCATGCC  
ACGGTCCGCANGANGCGCANACCCGCCAATGCCGAANCCACGAAACATCGGGCGCATCCACCTTCAACC

(SEQ ID NO. 34)

## Clone Rv116

:Rv116SP6.seq:::

ATACTCAAGCTTGGCCAGCCGTCGATGACAAGAAATATGTCGCAAAAGACTCAGCGGCCGACTTTGCTCGCAGCTGG  
CGGTACCGCGCCACCGAGTCGATGCCGTGGTCGCGGAAGAAATGCCTCCCGAATTGCGACGGCCAATTCCATTCCGGGA  
AGCATCCGCAATGCCAGCTGCGGTTGCCCCCTGCCGGCCACGGCACCCACTTGGCGCATGCGTCCACCTGGGCCAGC  
GCCCCGCCGCCAAATTCAAACAATAAAAATTGCACCCGGC (SEQ ID NO. 35)

.....Rv116T7.seq.....  
CCACCCGTGTATTTGGGATGGGCAAAAAGGCGAAGCACCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGG  
CTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGCTCGCCCTCCGACCGCGAACATTCTGGGG  
ATGGCAGCAACCTGGTAGCACCTGGCCGGGCGATGATCTGCAGCGTGGCCGGGGTAGTCCGCGCCCGGGCGGCTAC  
AGTCTGAAACGCGATGACCATCGATGTGTGGATGCAGCATCCGACGCAACGGTTCCTACACGGCGATATGTTTCGCCTC  
CCTGCCCGGT (SEQ ID NO. 36)

## Clone Rv117

.....Rv117SP6D2.seq.....  
CTGCCCATGTTTGGGGACGCCGACCGCGATGCTGGAGGCCTACACGGCCCTTGGTGCGCTGGCCACGGCGACCGA  
GCGGCTGCAACTGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCNGACCCCTNTCNCAANAGGATNTTGTTCGCC  
GGACCCCNCTC (SEQ ID NO. 37)

.....Rv117T7D4.seq.....  
CCGACTTTCCGCGGTACCCGCTCAACTTTGTGTCGACCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCA  
ACTTCATCCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTTCGGTCCACGATGACCCAGTACT  
ACATCATTCGCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGCGGGAACCCACTGGCGAACC  
TGTTTCAACCAAACTTGAAGGTGATTGTTAACCTGGGCTACGCGACCGCCTT (SEQ ID NO. 38)

## Clone Rv118

.....Rv118SP6.seq.....  
ATACTCAAGCTTGTACACCAAGTGTTCGACAGGCGCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCAGGT  
CGCCACCACGCTGGTCAGTGCGCGTTGCTGCGCTTGCAGCAGCCATTCCGGGGAATACTGCCCTGGCG  
CAGCTGGGGGATCCCAACTTCAATGGTTGCGGCACGGGTGTCAAATTCACGGTGGCGGTAGCCGTTGCCCTAATTGGA  
CCGCTCATCGCTGCTTTCGCGGTACCCGCGCCCGCACAGGGCTTCGGCTTCAGCCCCCATCAGGGCGGCAATAA  
CAAGAGCACC (SEQ ID NO. 39)

.....Rv118T7.seq.....  
GAGGCAGCTTCGCCGGCAATTCTACTAGCGAGAAGTCTGGCCCGATACGGATCTGACCGAAGTCGCTGCGGTGCAGCC  
CACCTCATTTGGCGATGGCGCCGACGATGGCGCCTGGACCGATCTTGTGCCGCTTGGCGACGGCGACGCGGTAGGTGG  
TCAAGTCCGGTCTACGCTTGGGCCTTTGCGGACGGTCCCGACGCTGGTCGCGGTTGCGCCGCGAAAGCGGCGGGTCGG  
GTGCCATCAGGAATGCCTCACCGCCGCGCACTGCACGGCCAGTGCCGCGGCGATGTGAGCCATCGGGACATCATGCT  
CGCGTTCATACTCCTCGACCACTCGGCGGAACAGCTCGATTCCCGGACCGCCAGCGCATTTGGTGATGGAATCGGCGA  
ACTTGGCCACCGCTGGGTGTTGACATCCTCGACGGTGGGCAATTGCGCCTCGGTAAGCTTTGCCGCGTAGCCTTTTC  
ATC (SEQ ID NO. 40)

## Clone Rv119

.....Rv119SP6.seq.....  
ATACTCAAGCTTCACTGACAAGGGACGAATTTCGTGGCCGCTGTTGCACTGGGTGGTGGCCGAGCTGGTCGCCACCA  
CTCAGGCCGCGGTACGGCGGTACCGCGCGGGAGCAAACTCGCGCGGGCATGGCCAACTTCTTGGCGACCATCACCG  
CAGACGCGCGCTTCGGACCCCTGCTGCCACCACACAGTTGGCCAACGCATTAATCACCCGCAAGCTTGGGGAATCCA  
CCGCCCTGTTTCGC (SEQ ID NO. 41)

.....Rv119T7.seq.....  
TCCATCACCCGATGTGGCNGGAGCACTGCCATGTGATCTCAACTACCACCTCCGGCCGTGGCGGTTGCGCGCCCCGG  
GGGTCCGCGCGAACTCGACGAGGCGGTGGGAGAAATCGCCANCACCCCGCTGAACCGCGACCAACCGCTGTGGGAGA  
TGTAATTCTGTTGAGGGGCTTGCCAACCAACCGGATCGCGGTGGTTGCCAAAATTCAACATGCGTTGGCTGACGGTGTG  
CCTCGGCAACATGATGGCAGGGGGATGGATCTGCCGCGGGACCGGAGGTGCGCCGCTATGTGCCTGACCCCGCTC  
CTACCAAGCGGCA (SEQ ID NO. 42)

## Clone Rv11

.....Rv11SP6.seq.....  
AGCTTTGCGATTGCTGAGTAATGTGCGCCAACGTACACAAACCGCGATGAATTCAATCATGCCGCCAGGGCGGGCA  
ACCAATGGTGGCCGCGAGCGGCGAGCTCGATCGCAGCGCGGAGGTTGCCGCGCCAGTTGATTACGAACAGGGTGA  
GGTCATAGGCGGGCAGGATAGTGACGAAGGCAAGACCTCCATCTGCCGTCGGAAGAAGTATCGAG (SEQ ID NO. 43)

.....Rv11T7.seq:.....  
AGCTTCAGAACAGGCCTGTTGTGGGCGCACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAAGTGCGGCCCGCACCG  
CCGGCATCTCCCGGTACGACAGGGCCGCGGCCCGCGCCGAGCGACGGCGTGTTCGCGCAGTTTCGCGTCAATGATGC  
TGACCTGATCGGCCACCCGGCGTTCTCGGCGTCTCGCGTTCACTAATCGCGGTGCTCAGCAGCGTCTCGACAGCCA  
CCACCCGAGTGGCGACCAGCTGCTCCACCACGGACCGCAGCGATGCCCCGTC (SEQ ID NO. 44)

## Clone Rv120

.....Rv120SP6.seq:.....  
ATACTCAAGCTTCAGTTCCTCCACGACGCGTTCCTCAATGAATTTCCCGATCCCAATCTCGGTTCAGATACAGGTC  
GCCATACCCCTTACTTCGGCAACGCTGGGCGGATTGGCCCTGCCGCTGCACCAACCATCAACGCCTTCAAATTGCCG  
GCAATCTCGTTCAGCCAATCCAT (SEQ ID NO. 45)

.....Rv120T7.seq:.....  
GCTCTACGCCGCTACGGGTGCAACATGCATCCCGAGCAGATGCTCGAGCGCGCACCCCACTCGCCGATGGCCGGAAC  
CGGCTGGTTACCCGGGTGGCGGCTGACGTTTCGGCGGCGAGGACATCNGCTGGGAAGGGGCGCTTGCCACCGTCTCNA  
AGACCCAAATTCGAAGGTGTTCTGCTGCTCTACGACATGACCCCGGCGGACGAGAAGAACCTTGACCGGTGGGAAGG  
CTCCGAGTTCGGTATCCACCAGAAGATCCGATGCCGCGTGGAGCGCATTTCTCGACACCACAACGGGATCCCGTCC  
TCG (SEQ ID NO. 46)

## Clone Rv121

.....Rv121SP6.seq:.....  
ATACTCAAGCTTGCCAAAGAGACCTCGTCCACCAAGCAGGACGCGACCGTCGAGGTGGCGATCCGGCTTGCGGTCGAC  
CCGCGTAAGGCAAAACAGATGGTTCGCGGCACGGTCAACCTGCCACACCGCACTGGTTAAGAACTGCCCGCGTCGC  
GGTTTTCGCGGTTGGTGAAAAGGCCAATGCCTGCGTTTGCCGTGGGGCGGATGTTGTGGGAGTGACAATCTGATCA  
AAAGGATTCAGGGCGGTTGGCTGGAATTCAATGCCGAATCGCGACACCGG (SEQ ID NO. 47)

.....Rv121T7.seq:.....  
CCACGCGTGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTGCGCGTTAGCGC  
CGGATTCACCATATCCCCTTGCGAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCATCGAGATAGTGGAGCA  
ACGCAATCCGTGCGGTACGGTTCGGGTCGTAATCGATGTGCGCGACCTTGCGGTTGACACCATCTTTGTCTATGCGGC  
GAAAGTCGATCATCCGGTAAGCGCGCTTATGACCGCCGCTTTGTGCCGGGTGGTAATCCGGCCATGCGCGTTGCGTC  
CACCGCAGCTGCAGCGGGCGCACACGCACTTCTCCGGGTTGACCGGTTNATCTC (SEQ ID NO. 48)

## Clone Rv122

.....Rv122SP6D2.seq:.....  
GCAGCATGACGGCGGTAGCGAACACCGCCGGATGCAGCGCAAGTAGCGTCGATGTGCTCACGGAATCGCCCCGGCACC  
GCGATCTCGANGATCACCAGTGCCACCCCTGCAGCGCNACACCGACGATTCCGTACACCGCCACGCGGATCAGGCC  
TGGGCCATCTGATTGGAGCTGGCGTANATGGCGGCGATGGTGACGATGGCCAGCGCCACATACATTGTGGCGGCCAGA  
ACCACGGCGTTGGGGCGGCGGTTCGATGAACACTAGGCGACGAGATCGCCCGGGGTCAACAGGTTGACCATCAGAAA  
CCTGCGACTAGCAGCGGCGGCCACTAGGAAGTACAAGAANGTGGCCACACCCCATCGAGGTAGGGTAAAGGCTGA  
TGGTCCCGAAATCGACTCCGGCCTAATACATGACTCTCTCTTTGCGTCATCGCCTTACTTGTGCGCGGAA  
(SEQ ID NO. 49)

## Clone Rv

.....Rv123SP6D2.seq:.....  
GGGACACACCTCGATGCTGCCGNATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGC  
TTCCGCCGCGGGCGTGACGCATCCCGTTGACCGGCCGGANCTCTCTA (SEQ ID NO. 50)

.....Rv123T7D4.seq:.....  
TGGGCGCCTCTTTGCGCCTTCCNNTTTAAACGNAGCANGACATTCTGGGTATCGAGTTGTACTGGATGGTGTGGCG  
ATGTCGGTGATCCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAGAGGAAATTGGG  
GCCGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTGACGCTGCCGGCATGGTGTTCGCC  
GTTACCATGTCGTTGTTGTGTTTCAGCGATTTGCGAATTATTGGTCAGATCGGTACCACCATCGCCTTCCC  
(SEQ ID NO. 51)

## Clone Rv124

.....Rv124SP6D2.seq:.....  
CCGATCGGCGCCGCANCTGGTTGGTGTTCGCGATGAATCCGCAGCGAAAATGTAGCTGCGGTGGCGTGTCTGACTCG  
TNGCGTCGACGCTCGTGGCAGCCACCGANCGGTTGGTCCAGGATCTGGATGGGCAAAGTTGTGCGGCCCGGCCGGT

ACGGCCGATGAGCTGACCGAGGTCGACAGCGCCGTGTTGGCTGACTTGGAAACCGACATGGAGTCGCCCCGGTTGGCGT  
CACCTCAAGCATTTCAATGGTTATGCGACCAAGTTTTTGGGTACGCCGTGACACATCACGTCGGGAGACTTGATGAGC  
TGTGTCTGCCAGATAGCCCCGAATCGGGACGACCGTGGTCACGGTGCGTCTGACCACTCGGGTCGGGTGCCCCGCGCT  
ATCGGCATGGGTGCGTNATCACAGCGACACGCGCTGCCAAGGANGTNCGGNCGGACC (SEQ ID NO. 52)

.....Rv124T7D4.seq:.....  
CGGGTTGCGGATCCACGCGTGCGGGTTGTCAGCAGCTACGGCACTGAACCGCGCCACAGCTCGCCGATCCGCTTTCG  
GTGGTTCTCGATCGACTCGCCGTAGGCGATGCGCAGCGCTGCTCGAATATCGGGTACACGTAGGCCGGCCTTCCNC  
TTTA (SEQ ID NO. 53)

Clone Rv126

.....Rv126SP6.seq:.....  
CTTGATTTTGATCATCATGACGATCATACCCTAATTTTGTACCCGCACTGGTTATCGTGGGTACCGTCGTGCTTTC  
CATGGGCGCCTTTTCGGGCTTCCGTATTGGTCTGGCAGGACATTCTGGGTATCGATTGTACTGGATGGTGGTGGC  
GATGTCGGTGATCCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCGGGTGAAAAAGGAAATTGG  
GGCCGGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGGAGTGGTGACGGCTGCCGGCATGGTGT  
(SEQ ID NO. 54)

.....Rv126T7.seq:.....  
GGGGATCCCTAGATCGACCTGCAGGCATGCAAGCTTGGCGTGCTTCCAACCCGAATTGGCTTTCGGCGCCATCGGT  
GAGGCGGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGG  
AACGCTTCCGCCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCG  
GAGNACTGTCAAGGCGGCGTGCCAGGTGCGCCGGGCGCACGGTGCGGACAAGGTGGTGCTGGCGGTCCCGATCGGCC  
CAGACGACATCGTGCGGAGATTGNCGGGTACGCCGATGAGGTGGTGTGTTTGGCGACGCCGGCGTNGTTCTTCGCCG  
NCGGGCANGGTTACCGCAACTTCACCCAGACCTCCGACGACGAGGTGGTGGCGTCTCCTGGATCGTGCTC  
(SEQ ID NO. 55)

Clone Rv127

.....Rv127SP6.seq:.....  
AAGGCTGCAGGTGCAAGCGGNTGGTTACGACTCCCTGTGTGTGATGGACCACTTCTACTATCTGCGTCTACACGGCCC  
TTGGTGCCTGGCCACGGCGACCGAGCGGTGCAACTGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCCGACC  
CTGCTGGCAAAGATNATCACCACGCTCGACGTGGTTAGCGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGCGGGTTT  
GAACGGAAACACCGCCAGCTCGGCTTCGAGTCCGGCACTTCCAGTGACCGGTTCAACCGGCTCGA (SEQ ID NO. 56)

.....Rv127T7.seq:.....  
CTTTCGGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTAGCTGCACTCCAATACTT  
CATCCTGACGCCGGAACAAATTGACGCGNGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACTACAT  
CATTCGCACGGAGAACCTGCCGCTGCTACAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGT  
TCAACCAAACCTTGAAGGTGATTGTTAACTGGGCTACGGCGACCCGGCTATGGTTATTTCGACCTCGCCGNCATGT  
TGCGACTCCGTTCCGGGTTGTTCCAGANGTCAGCCCGGTGCTCATCGCCGACGCTCTCGTCN (SEQ ID NO. 57)

Clone Rv128

.....Rv128SP6.seq:.....  
CGGTATAGCCCTCGGGTCCGGCCAGCACTCCGAGGCTTCGTGGGGTGGTCGCGACGCGCATGGGCCACCATCGCA  
TTCACCAAGTCTGCGCGAATCACCAGCACGTAGACGGTTCTTTCTAAGCAACACCGAAGTTTCACGACCCGAATGC  
TCCGGGAAACATGTACGGTAGGTCCGTATTCCGGCTACCGGCTGAGCATTGAGCACGCCGGCCAGCACCGCAGAGC  
CAGGCAATCAGCCGCGCCGACCGATCGCGGTGACCAGCTGAGTCTCCGAGACAATGCGGCCGGCACGCCGNNCTC  
CGGCGCACCGCTACNGCGCCCGTGG (SEQ ID NO. 58)

.....Rv128T7.seq:.....  
GTGATGGCACGCCACCGCGACACCACCGGCTGCGCTAQTTCGAGCCATACCGGGCGGAGCTACATCGGCTCGGCCGC  
CCAGTGTTCGGGCCCTCTTTCGAGGTCGAGGTGATACCGATTGCGCATCCGCANCCGNCCTGGACGACAGAACC  
GTGCCCTACGAGTGCTTGTGGGCGGGGCCAAAGAACAGCTTGGCATCCTGGCGGATTGGCCGGCGCGGCGTGGTC  
GCCAAGGACGACGCCGTTCCGGTGCTGATCGACGACGCGTGGGGTTACCGATCCGGAGCGACTATCAAGATGGGGG  
AGGTCTTGACACCATCGGCCCNACGGACATGTGATCGTGCCGACGTGCAGTCCCACCCG (SEQ ID NO. 59)

Clone Rv129

.....Rv129SP6.seq:.....  
GCGAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCATCGAGATAGTGGAGCAACGCAATCCGTGCGGTACGGT  
TCGGGTCTGACTCGATGTGCGCGACCTTGGCGTTGACACCATCTTGTGATTGCGGCGAAAGTCGATCATCCGGTNNG

CGCGCTTATGACCGCCGCCTTTGTGCCGGGTGGTAATCCGGCCATGCGCGTTGCGTCCACCGCGACCGTGCAGCGGGC  
GCACCAGCGACTTCTCCGGGGTTGACCGGGTGATCTCGGCGAAATCAGATACGCTGGCGCCGCGACGACCAGGCGTCG  
TGGGCTTGTNCTTGCGAATTGNCATGTCTAATCANGTCTTTCTCTCAGCTCTCGTCGCCGGGCTAGGCCGCATTGCC  
CTGCTCCTCCTCATCGCTTCGCTCTGCATCGTCCCCGGGCTAAGCCCGTGCCCCGAAA (SEQ ID NO. 60)

:::::::::::::Rv129T7.seq:::::::::::::  
GATGGTTGCGGGCACGGTCAACCTGCCACACGGCACTGGTAAGACTGCCCGCGTCGCGGTATTGCGGGTTGGTGAAAA  
GGCCGATGCTGCCGTTGCCGCGGGGGCGGATGTTGTGGGAGTGACGATCTGATCGAGAGGATTGAGGGCGGCTGGCT  
GGAATTCGATGCCGCGATCGCGAACACCGGATCAGAATGGCCAAAGTCGGTCGCATCGCTCGGGTGCTGGGTCCGCGC  
GGCCTGATGCCAACCCGAAAACCGGCACCGTCACCGCCGACTCCCCATGGCGTCCCGGATATCAAGGGCCGGCAAAAT  
CAACTTCCCGGTTGATCAGCAAGGCAACCTGCCTCCNCTCCGG (SEQ ID NO. 61)

Clone Rv130

:::::::::::::Rv130SP6.seq:::::::::::::  
ATACTCAAGCTTCGTATAAGACCATGGTGCGCTTCTTTACCCCGTCCAGAGTCGGGGGCATCCGCACCGGCTCGCA  
TCGCATCATCTCCACGACGGGCGCTCATCAGCTTGGGCCATTTCAATGTACTTGATACCCCGCGCTGCGGGTAGG  
CCACTGCGACAATTCAAACACGGTGTACACGGTGAATAGTGTGAGATGGGCTCTGATCAACCGTCGCAAACCCGGT  
TTCGCATCAATAGCGGAATCCACCGGGTTGCATGGAGGCTGCTGACCTTGGAACCAAAATTTTTTCATTACAACAA  
AACAAACGCCNCNGAAACTTTGCA (SEQ ID NO. 62)

:::::::::::::Rv130T7.seq:::::::::::::  
CGAATTCGGCGTGACACCGCTATGGGTTGCAGCAGCGGCTGGCGCCGCACACCCCACTGGCCCGGGTGTTTTCGCCCCG  
AACCCGGATCATGGTGAGCGAAAAGGAGATTGCGCTGTTCGATGCTGGGATTGCCACCGCGAGGCCATCGACCGATT  
ACTCGCCACCGGGGTGCGAGAGGTGCCGCACTCCCGCTCCGTCGACGTCTCCGACGATCCATCCGGCTTCGCGCTCG  
GGTGGCGGTAGCCGTGATGAAATCGCTGCCGGCCGCTACCTGCAAGGTGATTCTGTCCCGTTGTGTGCAAGTGCCTT  
TCGCGATCGACTTTCCGTTGACCTACCGGCTGGGGCGTCGGCACAACACCCCGGTGAGGTGCTTTTTGTTGCAATTGG  
GCGGAATCCGTGCTCTGGGTTACAGCCCCGAACCTCGTCACGGCGGTGCGCGCCGACGGAGTTGTTATCACCGATCCGT  
TGGCCGTACCGCGCCTTGGGC (SEQ ID NO. 63)

Clone Rv132

:::::::::::::Rv132SP6.seq:::::::::::::  
TCAGACTCCACCCAGCCAGCAGGCAGCGCGAAGCTGAATCCTCCAACCGGGTTGTCGATCCGGACAGGTTGGGGTGCG  
TTTGGGGCAATGACAGGTGGCGGCGGTGCGTTCCGGTTCGGCCGGCGGAGGTGCTGCGTTGGGATCGCCCGGCTGGGCA  
TTCNGCGTGTGGCGGCGGCGGTGGTGGGGGGGCAACAGGTGTGCGCGGTGCGGGTGCGGCTGCAGCGGTGACGGC  
GGCGAAGCGGCCGTTGTGGGTACCGGGGGCGCTGGCTCCGGATCGGCGTTGGCGGTGCGGGGCACCGCAACGGTCACC  
AAGCTGGCGCTGGCCATCGCCGCGATAGCCAGTGCCGCCAATCGTCCCTTGCGACGTGTCAAGTNGGGGTCCACCTGA  
TGCATGGCCAAAGAACCTACCGTGTAAACGGCNAACNCAAGGACCGCGCGGTGCGN (SEQ ID NO. 64)

:::::::::::::Rv132T7.seq:::::::::::::  
TTTCCGCGGTACCCGCTCAACTTTGTGTCNACCCTCAACGCCATTGCCGGCACCTACTACGTNCACTCCAACCTACTTC  
ATCCTGACGCCGGAACAAATTGACGCGAGCGGTCGCTGAACAATTCCGTCCGTCCCACGAAAGAACCAGTTTTNCNT  
CTTTCNACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCCTGTG  
TTTCAACCAACACTTAGAGTGTAATTGTAAACCTGGGCTAGGGGAAACCGGCTCTAGTTTTTCCACCNTCTCCGCCCC  
NTGTTTCGAATACTCCGTTCCGGTTGTCCCCAAA (SEQ ID NO. 65)

Clone Rv134

:::::::::::::Rv134SP6.seq:::::::::::::  
GCTTCCGGCTCGTATGTTGTGTGAATTGTGACCGGATACCAATTCACACAGGAAACAGCTATGACCATGATTACGC  
CAAGCTAGTTAGGTGACACTATACTCAAGCTTGCCGGCTGGTGGGCGGACCACTTCGATGGCAGACCCGTTGA  
ACTGCTGCCCGGCAATTCTTCTTGGTCGCCCCGGACCGATGGACCGCGCTGGGATTCCAGAAGGTGCCCGATCCCGC  
CCCTGGGAAAACCGCGTGCACCTCTACTTCACGACCAACGAC (SEQ ID NO. 66)

:::::::::::::Rv134T7.seq:::::::::::::  
CCGATCGACTGATGCGCCGACAACCACGCCCCAACAACTGGAATGAACCGTCGTGACCATCATCAGCACGCGGTTGTA  
GGCGACTTGCGACATGTTCAACCCGCGTACTCGGACGGAATCTTCAAACCGAAACAGCCAGCTCGGCCAGGCCTTT  
CACGTACTCGTCGGGGATCTGGGCACACGCTCGAGGACGCTGCCGTCCACGGTGTCTAGGAATTCGCCGAGTTTGAC  
CAGAAACGCTCGGTTCCGGCCCTCCTCGGCGTCCGACGGCTTGGGAAATGGGTGTATGAGCCCTACGGGAAACCGGCC  
CACAAAGAGTTCTTTGGCGAAGGACGGTTTATCCCAACCACTTTTCGCGAGATTCTCGGCAAGGGCCCGCGCTTGCTC  
CTCGGTGACCTGAGTTTGCTGTGCCATCGCCGCTCCTCCCTGA (SEQ ID NO. 67)



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:::Rv135SP6.seq:::

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(SEQ ID NO. 68)

::::::::::Rv135T7.seq::::::::::

(SEQ ID NO. 69)

.....Rv136SP6.seq.....

01

.....Rv136T7.seq.....

(SEQ ID NO. 71)

.....Rv137SP6.seq:.....

2)

.....Rv137T7.seq.....

(SEQ ID NO. 73)

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##### Rv138
:::::::::::::Rv138SP6.seq:::::::::::::

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(SEQ ID NO. 74)

(SEQ ID NO. 74)

.....Rv138T7.seq:.....  
CAGGCATGCAAGCTTTCGTCAAGTTCATTGCGCCAGCAGACCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGG  
CCAACGGTGATTTCTTGGCCGCGCTGACGGCGCGAACGACGCCAGCGACCACATTAGCAGATGGCCAGCGCGTGCC  
GGGCCACGAGGTTGGTGCTCGGCGGCTACTCCCAGGGTGCGGCGGTGATCGACATCGTCACCGCCGCACTGCCCCG  
GCCTCGGGTTCACGCAGCCGTGCGCGCCGCGAGCGGACGATCACATCGCCGCGATCGCCCTGTTTCGGGAATCCCTCGG  
GCCGCGCTGGCGGGCTGATGAGCGCCCTGACCCCTCAATTGCGGTCCAAGAACATCAACCTCTGCAACAACGGCGACC  
CATTTGTTTCGGACGGCAACCGGTGGCAACGCACCTAAGCTACTTGCCCGGGATGA (SEQ ID NO. 75)

## Clone Rv139

.....Rv139SP6.seq:.....  
GTTTATGCACCTGGTTAGGTGTTCCATGAGTTTCATTCTGAACATCCTTTAATCATTGCTTTTTCGTTTTTTTATTAA  
TCTTGCAATTTACTGCAAAGCAACAACAAATCGCAAAGTCATCAAAAAACCGCAAAGTTGTTTAAAAATAAGAGCAAC  
ACGTACACAAGGAGATAAGAAGAGCACATACCTCAGTCACTTATTATCACTAGCGCCCGCCGAGCCGTGTAACCGAG  
CATAGCGAGCGAACTGGCGAGGAAGCAAGAAGAACTGTTCTGTGATAGCTCTTACGCTCAGCGCAAGAAGAAATA  
TCCACCGTGGGAAAAACTCCAGGTAGAGGTAC (SEQ ID NO. 76)

## Clone Rv13

.....Rv13SP6.seq:.....  
ATACTCAAGCTTGGGTGTAGCCGATCACCGGAAGTCNCATGATCAGCCACGTTCCGCGCCGCCCGGCATACGGTGGTG  
TACCGATCTCCGCGTCATACACCCGCGGGTAATCGCCGACGGTGCCGGTTCGCGAGCCGAA (SEQ ID NO. 77)

.....Rv13T7.seq:.....  
AGCTTTATCGAAAGCGCGAACAGCTCGCGGGCGGCCACGAGCTGCTGCGTCGGATTGCCGGCGGGCAGATCAATTCCA  
GGCAGCTCCCGGACAATGCGGCTCTGCTGGCCCGCAACGAAGGACTCGAGGTCACCCCGGTGCCCGGGTTCGTGGTGC  
ACCTGCCGATCGCACAGGTTGGCCCAACCGGCCGCTTGATGCCGGTTCGGCAAGCCCGGCAGTTGCCAAACCCATC  
GTGATCAGGCTCGGCTCGCGAGTTTCGGCGAAGAAATGGTTCGCCTGATCACCTACCATCGGCCA (SEQ ID NO. 78)

## Clone Rv140

.....Rv140SP6.seq:.....  
TCAACACGCCGCCAGCCACCACGCGCGGGTTCGGGCGCCGGGCCCCGGGCTCCAGGCTNCTCCGCTCGGTGATGGCAGC  
CCACCGCGACACCACCCGGCTGCGCTACGTCGAGCCATACCGGGCGGAGCTACATCGGCCCGGGCGCCAGTGTTCGG  
GCCCTCCGCCAGGTTCGAGGTCGACACCGATTTGCGCATCCGACGCGCACCTGCGACGACAGAACCAGCGGCCCTA  
CCCACTGCTGTGCGGGCGGGGCCAAAGAACCAGCTTGNCATCCTGCCACAATTGGCCGGCGCCCG (SEQ ID NO. 79)

.....Rv140T7.seq:.....  
CAGGCATGCAAGCTTCACGTCCGTACGGCTCGGGTACGCTTCGGTTCGAGTGTGCGAGTGATAGATGACGACCGGGAC  
CTCGTCGGCATCTTCCATAGCCCGCCACACCTTCAGTTGCTCACCAGGAATCCAACCGGTAGAAGGTTCGGCCAGCGCTC  
GGCATTTGGTCATCGGGATATGCCGCTCGGGACGGTCAGAGCCCTCGGGTCCGGCCAGCACTCCGAGGCTTCGTTCGG  
GTGGTCGCGACGCGCATGGGCCACCATCGCATTCACCAGGTCTGCGCGAATCACCAGCACGTAGACGGTTCCTTTCT  
AAGCAACAC (SEQ ID NO. 80)

## Clone Rv141

.....Rv141SP6.seq:.....  
AATATTCAAGCTTTTCGGCGGAAACGGACNCCTTGCGAACATTGATAACAAAATAGAAATCATTGATGGTTTTGAGTCAC  
CAGGCCGATCAAGCCTTCGCCGAGCCAAATTCGAATCAAGAGGCCAAGCCCGTACCAATCAGCCCGGCAACGAGGGA  
TTCCGTCNTTATCAGCCNAAATAACTGCTCTCGGGTACCACCCAAACAGCGCAATATGGCGAAAAACGGTCGCCGTTG  
CACAACTATAATGTCTCGGTATTGTTGATTAAAAAGATACCCACCACAGGGCAATCCAATGAGAGCGGTAAATT  
GACCGTAAAAACCTCCCGTCATCTGTTT (SEQ ID NO. 81)

.....Rv141T7.seq:.....  
CAGGCATGCAAGCTTGCTGCATCTTCTGTGACTGCTCCCGAAACCTGGGGGTGTGCTGCTGTGTATGCACGGCATA  
CGGACATCCTTCCCCTGATACCCGCGGTGCAACCAGCCACGTGTCCATCATCAGGGGTCAACCCCGGCCAAGGGCGAC  
GGCAGCCCAAGTTCGCCGACCGTTAACCTAGTGCTGTTAGCTTCATTTGCTGCGAGCAAAACAGCTGGTTCGGCCGTTA  
GGAATGAATTGAAACTCAACCGATTGGTGCCGCGCTAAGTGCTCTGCGGGTGCGCTGGTGTGTCCGCGTGT  
GGTAACGACGACAATGTGACCGGGGAGGTGCAACCACTGGCCAGGCGTCCGCGAAAGTCCATTGCNNGGGGAAGAAG  
ACAC (SEQ ID NO. 82)

## Clone Rv142

.....Rv142IS1081.seq:.....  
GAAAGTGCCCAAGGTGTTGGTGAAACTCGTGGACGGTCCCCAGGATGTTGGCAGCACATTCACCGGACATGACCGG  
AGCAAGACCGGACATCCTCCCATACCGTCGTGCGCGTGACATCCGTAGCCCGTCCTGGCAGGTGCTGGGTTGAACAA  
AATCAGCCCAACACCTGCCACGACGAAGAAGCGGGTTGCGCTGGCATGTTCTTGTGCGCTCGGCGATCGAATTCACGA  
ATTCTTATCTACGGGACCGTGC GGCGCTGGTGTTCACCGTGTCTTCCCACACCTGGATCCCACGGTGGCCGC  
CTGGCCCTCAAGGGGACATTTGCTGTGGCGTTCTATCCCGGCCGTTTCGGCGCGGCCGCTTTTGGATACTTTGGAGA  
CCGCCTCGGCCGCCAGAAGACCCTGGTGCACACACTGTTGATCATGGGCCTGGCAACCGTGACTGTTGGGCTGGTTCC  
ACGACAGTGGCCATCGCGC (SEQ ID NO. 83)

.....Rv142SP6.seq:.....  
ATATTCAAGCTTTGTACACCAAGTGTTCGACCAANCGCTCCATCCGGCGAGTGGATACTCCCAGCAGGTAGCAGGT  
CGCCACCACGCTGGTCAGTGC GGCTTCATCTCGCTTGGCGCGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTGGCG  
CAGCTTGGGGATCGCGACGTCGATGGTTGCGGCACGGGTGTCGAAATCACGGTGGCGGTAGCCGTTGCGCTGATTGGA  
CCGCTCATCGCTGCGTTCGGGTAGCCNCCCCGCACAGGGCGTTCGGCTTCAGCCCCATCCAAGGCGGCGATGAACG  
TCGAGAGCAGCCCGCGCAGCAAATCCGGGCTCGCTGTGCGAGTTGGTCAGCCAGAAGCTGCTCGGTGTCATAAGATG  
AGAAGAGGTGAGTGCCTTCCTTCG (SEQ ID NO. 84)

.....Rv142T7.seq:.....  
CAGGCATGCAAGCTTTTGGCTGCGCGGGCAGCTTCGCGGCAATTCTACTAGCGAGAAGTCTGGCCCGATACG  
GATCTGACCGAAGTCGCTGCGGTGCAGCCACCTCATTTGGCGATGGCGCCGACGATGGCGCTGGACCGATCTTGTG  
CCGCTTGCCGACGGCGACGCGGTAGGTGGTCAAGTCCGGTCTACGCTTGGGCCTTTGCGGACGGTCCCGACGCTGGTC  
GCGGTTGCGCCGCCAAAGCGCGGGTCGGGTGCCATCATGAATGCCTCACCGCCGCCGACTGCACGGCCAGTGCCCC  
GGCGATGTCAGCCATCGGGACATCATGCTGCGCTTCATACTCCTCGACAGTCCGCGGAACAGCTCCATTCCCGGACC  
GCCCCAAGC (SEQ ID NO. 85)

## Clone Rv143

.....Rv143SP6.seq:.....  
ATACTCAAGCTTTTGGCTGGGTGCGCTTCCAATTACGGCTGCACCGCTATGGGTTGCAGCAGCGGCTGGCNCCGCACA  
CCCCACTGGCCCGGGTGTTCGCCCCGAACCCGGATCATGGTGAGCGAAAAGGAGATTCNCTGTTGATGCTGGGA  
TTCGCCACCGCGAGGCCATCGACCGATTACTCGCCACCGGGGTGCGAGAGGTGCCGCGATCCCGCTCCGTGACGCTCT  
CCGACGATCCATCCGGCTTCGCGCGTGGGTGGCGGTAGCCGTGATGAAATCGCTGCCGGCCGCTACCACAAGGTGA  
TTCTGTCCCGTTGTTCCAGTGCTTTTCGCGATCGACTTTCGTTGACCTACCGGTGGGGCGTGGGCACAACACCC  
CGGTGAGGTGTTTTTGTGAGTTGGGCGGAATCCGTGCTCTGGGTTACAGCCCCGAACCTCGTCACGGCGGTGCGCC  
GCCGAC (SEQ ID NO. 86)

.....Rv143T7.seq:.....  
CAGGCATGCAAGCTTCAACCTATTGACGATTGTGCGAACTGACGGCGCCCGCGCATGGCCATCCGGAAGACCATCA  
TTGGCCAGTGGCCGGCGCTAACAGGTTCCAGCCCCCACCAGTGCCGCTCGAACATGCGGTGCAACCCATTGCGAGG  
CCGGCAGGGAAAGCACCGCGGAAGCCGCAAGGGGTGCAAGTTCCGCGCCCAATAGTGCTCGTCCGCAACCAGATGCGCT  
CGAAAACCGCCGCCGCGAGTCAGCGCACCCGACGCGAGGTGAGAGACGTCGTACGCGCGCCACATGGGGTGCCAT  
CGGCACGGCAGGTAGGCCGCGCGCAACCCCAACGCGTGGTGCATGCCACGGTCCGCGAGAGGCCACCAACC

(SEQ ID NO. 87)

## Clone Rv144

.....Rv144SP6.seq:.....  
ATACTCAAGCTTCCCGCCGCGAGTGACGGCGCGCCTAGCGCCACTTGATGCCGCACCCGATCGACGGNCGTTGGTC  
GGGTTGACTGGCCGCCCGCGGAGCAGGGCGTCAACCGCGCGCCCGACGTCGGCGGCCGTCACCGGTGCGCCATTGCC  
CGGGCGGGAGTCGTGAGCTGACCACGGTAGACAAGTCGGCGCTGGCCGTGGAAGACAAACGTGTGGGTGTGAGGC  
CGCGGAGAAGGCGNCGCGACGTCCTCGGGTTTCGTGATAGAGATACGGGAACGTCCAGCCGTGGCGGGCGGGCTCGGC  
GACCATCTGATCGGGCCCGTCTGCGGGTAGGTGACCACGTCCTTACTGGAGATACCGACCATCGGGACCCTTTGATC  
GGCGAGGTCCCGGCCGACCGTGGCCAATCCGGCGCGACGTCGCGCCGTACCGGCCAGTGTT (SEQ ID NO. 88)

.....Rv144T7.seq:.....  
CAGGCATGCAAGCTTTANCANATCAACCCCGCCCCGCACCGACCGACGATGTCGATGCCATCGAGGTGAATGT  
CGAAGTGGCNCAAACCATCTGGCGACCGCGACCAACCGGCAACATGGGTACCGGCGATTTCGGGTGCCAATGCCGACCC  
GACGGCCGCTCTACCGCAGGTGACCTCGATCACCAGACAGCGCGCGCTTATACTACGCACCCCTACCGTGTCA  
CGCCAAACCGCGCTGGTGGTCGATTGCCGAGTGACACCCCGCACCCAGTGTGTCGCCCGGATCCGCCGACCAATCC  
CGCACCCACGTCGCCAAACCCGAAATCACCGTGATGCCGTGGTAACTGACCACCGACAGTAACGTCACTACGGCCGCC  
ACGCCGACGCCGAACCAACACGCACATGATGATCGGCTG (SEQ ID NO. 89)

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:::Rv145SP6.seq:::

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.....Rv145T7.seq.....

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:::Rv146SP6.seq:::

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.....Rv146T7.seq:.....

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:::Rv147SP6.seq:::

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(SEQ ID NO. 94)

.....Rv147T7.seq.....

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:.....Rv148SP6.seq:.....

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.....Rv148T7.seq.....

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CAGGCATGCAAGCTTGGCGTGCCGTTCCAACCCGAATTGGCTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTC  
 AACGACGACGTCGTCGCTGGACACACTCGATGCTGCCGCCATGGACGCGGTGGAACGCAAGCAGCTGATCGAGCTA  
 CAACGCGCGCGCGGAACGCTTCCGCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGAC  
 GGCATCGCCACCGGAGCGACGGCCAAAGCGGGCTGCCAGGTGCGCCGGGCGCACGGTGCGGACAAGTGCTGCTGGCG  
 TTTCCGATCGCGCCAGACGACATCGTGGCGAGATTGCGCGGGTACGCGGATGAAGTGGTGTGTGTTGGCGACCCGGCG  
 TTGTT (SEQ ID NO. 97)

## Clone Rv149

:::Rv149SP6.seq:::

ATACTCAAGCTTTGGCATTGTGCACATTTTCCACCCGTGCTCTATTAATGCTGAGCCGCTAATTGTGACCCCAAGTCGG  
GAAACACGCGGAGCACCAAATTCACCGCAGCGCGCGGGGCGGTTCAACTCACCATGGATCGCTCTCGTCGTCTGGTGC  
TGGACAATCGTCGCTGTAGCGCGTCGCGAACACCTCAGCTTCTGCTGCCGCGGCTTCTTCCGGCGATGGTAACCCCA  
GGTTTCGCCCACGGTCTTACGTAGCAGTGCGACGCGGTGTTTCATCTGCATCGACCTGTTGACTCATCTGTCAAGGAT  
GAAGGCGTACTGGGCCGACTGCGCTTCTGCCGCGCCAGGTGCGCAATCACCAGGATCTCAGAAACGAGCTGCGACTC  
ACTCTTCCAGGCCACCCTGGCCGAAAGCTCGACATGGTCAATCCGGCCG (SEQ ID NO. 98)

:::Rv149T7.seq:::

CAGGCATGCAAGCTTGC GGCGCGGAGTGGTTTCGACGGCCGCTCGCTTCTCGGCATCGGTTTGGGCTGTCAACAGCAG  
TTGGTAGTTCTTACGTAATGTTGTTTCGAGCGTCGAGCCGCGCGCTGTCGAGGTGCGCGGACGCGTATCCCGCCAG  
GCCGGTCAGGGTGCCCTTCCAGTCCACGCGCGTGTGGTCGGCGAACCCTTATCTTCAATCGAGACGATCGCCAGCTT  
CATCGTGTGGCGATCTTGTCCGAGGGCACCTCGAACGGCGCTGCGAGTACAGCCACGCGATCGTGTGCCCTTCGC  
GTCGACCATCGTCGATACCGCAGGCACTTGCCCTC (SEQ ID NO. 99)

## Clone Rv14

:::Rv14SP6.seq:::

ATACTCAAGCTTCCCGCGCGCCAGTACCGAAAGCGCGAACAGCTCGCGGCAGCCACGACGTGCTGCGTCGGATTGCC  
GGCGGCGAAATCAATTCAGGCAGCTCCCGACAATGCGGCTCTGCTGGCCCGCAACGAAGGACTCGAGGTACCCCCG  
GTGCCCCGGGTCGTGGTGCACCTGCCGATCGCACAGGTTGGCCCAACCGGCCGCTTGATGCCCGGTGGCAAGCC  
GGCAGTTGCCAAACCCAGCGTGATCAGGCTCGGCTCGCGAGTTCGGCGAAGAAGTGGCTCGCCTGATCACCTACCATC  
GGCCAGGATCTGCGTGTGCATCACAACGCTCGCAAGGAGGTTGTTGTGGTGTATCGACGGCCTTTAGCCAGATGTT  
GGAATCGACTATCCGATAGTGTCCGCGCAATGGACTTGATCGCCG (SEQ ID NO. 100)

:::Rv14T7.seq:::

AGCTTCGGTGTAGCCGATCACCAGGAGCCGATGATCAGCCACGTTTCGCGCCGCCCGGCATACGGCGGCGTACCGAT  
CTCCGCGTCATACACCCGCGGGTAATCGCCGACGGTGCCGGTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAG  
TTCCAGGTCCAGCGGGTGGCGCAGCAACGGCGCGAGCTCAACGACGTCAATCAGGTTGTGCTTTCTACGGTCACCGA  
CCCGGTGACCGTAGTCGCCCCGGTGCGCTCGGCCGAGAAGTTGCACCGCCACCACCGGACACCGTCTTGACGCGGAC  
GCCACCCCGGATCGGTTGTTGGCCAAGGTAATTGGGTATTCCATTGACGGGACGCCGACCCCGCAGCCCCAGTAC  
CGCCACGACCACGCGGCTGACCCACCACTGTACGAACACCAAGGCGACGCCG (SEQ ID NO. 101)

## Clone Rv15

:::Rv150SP6.seq:::

ATACTCAAGCTTCGGTGGCTTCGCCCGCCCTGCCGGGTGGACTTCATGACAACGCGGGGGCGATTACCCCCGCTACCG  
CCAGCAGCATCAGCGCGGTACCTAACACCGCCCGGATGCCTCGCACGTGCCCTCGATGTGCTCAGGGAATCGCCCCGGC  
ACCGCATCTCAGGATCACCAGGTTACCCCCGGCAGCGCGACACCGACAATTCGTAACCCGCCACGCCGATCCGG  
CCCTGGGCCAGCTGATTGGAGCTGGCG (SEQ ID NO. 102)

:::Rv150T7.seq:::

CAGGCATGCAAGCTTCCACATGTACGGATCCACGAACATCCCGTTGAACTGACAGGTGCGGGCCGGCTCGATCAGGCC  
GGCCACTTGTCTACGCGGTTACCGAAGATCTCTTCGGTGACCTGCCCGCCGCGGCCAGCTCGGCCAGTGCCCCGGC  
GTTGGCCGCGCGGCGACGATCTTGGCGTCCACGGTGGTCCGGGCTTGTCCCGCTAGCACGATCCGCGAGTCGSCCG  
TCACCCGGGT (SEQ ID NO. 103)

## Clone Rv151

:::Rv151SP6.seq:::

ATACTCAAGCTTTCCAAGTCCAAGTGTGATCATGGCCAAAGAGCTCGACAAAGCCGTAGAGGCGTTTCGGACCCGC  
CCGCTCGATGCCGGCCGTATACCTTCTCGCCGCCGACGCCCTGGTGCTCAAGGTGCGCGAGGCAGGCCGCGTCGTC  
GGGGTGACACCTTGATCGCCACCGGCGTCAACGCCGAGGGTACCGAAAGATCCTGGGCATCCAGGTACCTCCGCC  
GAAGACGGGGCGGCTGGCTGGCGTTCTTCCGCGACCTGGTCGCCCCGCGGCTGTCCGGGGTCGCGCTGGTACCAGC  
GACGCCACGCGGCGCTGGTGCCGCGATCGGGGCCACCCTGCCCGCAGCGGCTGGCAGCGCT (SEQ ID NO. 104)

:::Rv151T7.seq:::

CAGGCATGCAAGCTTCAACGTAGGCGCCGTCGATAAATGACTCCGCCGCGCTTCGCACATCCTCGTAGCGATCCTTG  
GCGAGCAGGTCAACGGGCGCTGCCGTCGAGGAGCCGGTTTGGCGTGCAGCCACTGGCCGACACCTCGGGGGTA  
AGCGAATCCGAGAGCAGGAGGACGAGGTACGAAGCTGCGCCAGCCGGTCTACCGCTCAGGGCGGATGTCGCCGGTC  
CGCCACCCGCGTACCGCCGATCGGACACCTGTATGACGCGGCGACGTC (SEQ ID NO. 105)

## Clone Rv152

.....Rv152SP6.seq:.....  
CGCGGCGGCGCATTACCCCCGCTACCGTCAGCAGCTTGACGGCGGTAGCGAACACCGCCGGATGCAGCGCAGGTGCGT  
CTATGTGCACACGGAATCGCCCCGGCACCGCGATCTCGAGGATCACCAGTGCCCGCCCCCTG (SEQ ID NO. 106)

.....Rv152T7.seq:.....  
GGGATCGAGGAACAGCGCGTTGAACTGATAGGTGCGGCCCGGCTCGAGCAGGCCGGCCATTGTTCGATGCGGTTACC  
GAAGATCTCTTCGGTGACCTGCCCCGCCCGCCGAGCTCGGCCAGTGCCCGGCGTTGGCCGCCGCGGCGACGATCTT  
GGCGTCCACGGTGGTCGGGGTCATGCCCGCGAGCAGGATCGGCGAGCGGCCGGTCAGCCGGGTGAACTTCGTTCGAGAG  
CTTGACCTGCCGTGCGGGAGGCGAACACGGTCGGTGCGTATCTCGACCAGGCCCGGGCAACCTCGGGGGTGGCGCC  
GACGGTGAACAGGTTGCGCTGGCCACCGCGGGTAGCCGCCGGCACTATGCCGATGCCAGGCCGCGGATCACCGGTGC  
GGTCAGTCGGGTCAGGATGTCGCCCGGCCCGAGGTCGAAGATCCAGCGGGCGCGGCCGCGTGGACACNGGTGATCTC  
GTCCACCATCGACTTTCGTGATCA (SEQ ID NO. 107)

## Clone Rv153

.....Rv153SP6.seq:.....  
TAACTCAAGGCTTGCGTTGAGGCCCCAGGCCCATCGACGGTTTGGCGGCCTTAAATGCACTGAGGTGCTCAATTGACC  
CCACAGCGGAAATGCCGACTATTGCGAGGCTCCTTCGCCTTGCTGCCGAGAGGGGCTCCGCGGGAACCGCATGCA  
GGTATATGACCTCGGTTTCTCGGGTGCTACCGCGTGCCCTGTGCGAGGATGAACTCGGCGTTGGAATTGTCCAGCCGGC  
CCAATTCATCGAGCGCAGATTGCTACACATGGCCGGCGGCGACATACGCTTACCCTGGATCTGCTCCACACGGACCG  
CCCTGTGCGGATCCTGCTCACGGGTAAAGGAACTTACNTGGCNCTCGGTGCC (SEQ ID NO. 108)

.....Rv153T7.seq:.....  
CCTTCTGCGCCACCCACACCGTCAACGCCCGCGAAGTCGACGTCGTCCAGGCCATCGGCGGCCTCACGGATGGATTGCG  
GCGCGGACGTGGTGATCGACGCCGTGCGCCGACCGGAAACCTACCAGCAGGCCCTTACGCCCGCGATCTCGCCGGAA  
CCGTTGTGCTGGTGGGTGTGCCGACGCCCGACATGCGCCTGGACATGCCGCTGGTCTGCTCTCACGGCGGTG  
CGCTGAAGTCGTGCTGGTACGGCGATTGCCGCGCCGAAAGCGACTTCCCCACGCTGATCGACCTTGACCTGCATGGCC  
GGCTGCCGCTGCAGCGGTTGCTTCCGAACGCATCGGGCTCGAAGACGTCGAGGAGGCGTTCCACAAGATGCATGGCG  
GCAAGGTATTGCGTTCGGTGGTGATGTTGTGATGGCCGCCATCGAGCGCGTCATCACCACGG (SEQ ID NO. 109)

## Clone Rv154

.....Rv154SP6.seq:.....  
ATACTCAAGCTTGATTTTGATCATCATGATGATCATCACCCGAAGTGTGGTAGCCGAGTGGGTTATCGTGGGTACCGT  
CGTGCTTTCCATGGGCGCCTCTTTGCGGCTTTCGCTATTGGTCTGGCAGGACATTTGGGTATCGAGTTGTACTGGAT  
GGTGTGGCGATGTCGGTGATCCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAAA  
AGAAATTGGGGCCGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCAGGGGAGTGTTACCCTGCCGGCAT  
GGTGTTCGCCGTTACCA (SEQ ID NO. 110)

.....Rv154T7.seq:.....  
ATTGNCTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCGTCCGCGGGACACACCTCGATGC  
TGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCCGCCGCGGGCGTGA  
CCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCGGAGCGACGGCCAAGGCGGCGTG  
CCAGGTCGCCCCGGGCGACGGTGCGGACAAGGTGGTGCTGGCGGTCCCGATCGGCCAGACGACATCGTGGCGAGATT  
CGCCGGGTACGCCGATGAGGTGGTGTGTTGCGGACGCCGGCGTTGTTCTTCGCCGTGCGGCAGGGTTACCGCAACTT  
CACCAGACCTCCGACGAAGAAGTGGTGGCGTTTTCTGGATCGTGCTC (SEQ ID NO. 111)

## Clone Rv155

.....Rv155SP6.seq:.....  
ATACTCAAGCTTTTCCCGTCCGTCATCGCCCAAGCGCGTGAGGCCGAAGCGGCTGGTTACGACTCCCTGTTTGTGATG  
GACCACTTCTACCAACTGCCCATGTTGGGGACGCCCCGACCGCCGATGCTGGAGGCCTACACGGCCCTTGGTGCGCTG  
GCCACGGCGACCGAGCGGCTGCAACTGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCGACCTGCTGGCAAAG  
ATCATACCACGCTCGACGTGGTTAGCGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGTTGGTTTGGAGTGGAAACAC  
CGCCAGCTCGGCTTCGAGTTCGGCACTTTCAGTGACCGGTTCAACCGGCTCGAANAGGCGCTACAGATCCTCGAGCCA  
ATGGTCAAGGGTGAGCGCCAACGTTTTTCGGCGATTGGTACCCACCGA (SEQ ID NO. 112)

.....Rv155T7.seq:.....  
CGGCCACCGGGGCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCCGACTTTC  
CGCGGTACCCGCTCAACTTTGTGTCGACCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAACTACTTCATCC  
TGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACTACATCATTC

GCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAAC  
CAAACCTGAAGGTGATTGTTAACCTGGGCTACGGCGACCCGGCCTATGGTTATTCGACCTCGCCGCCCAATGTTGCGA  
CTCCGTTCCGGTTGTTCCAGAGGTCAGCCCGGTCTCATCGCCGACGCTCTCGTCGCCGGGACCAGCAGGGAATCGG  
CGATTTGCGCTACA (SEQ ID NO. 113)

## Clone Rv156

:Rv156SP6.seq::

ATACTCAAGCTTGGGGTGGCGCTGTCGGTCCGTGTGCTTGGCGGCGTCCGTATCAACACCGCCACGAAATGGGGCAC  
AAGAAGGATTCGCTGGAGCGGTGGCTGTCCAAATCACCTCGCCAGACCTGCTACGGGCACTTCTACATCGAGCAC  
AACCGTGGCCATCACNTCCGGGTGTCCACACCGGAGGACCCGGCGTCCGGCGGGTTCGGCGAAACGTTGTGGGAGTTC  
CTGCCCCGAGTGTATCGGCGGCTTGCCTCGGCCGTTTCAATTTGGAGGCCCAACGGCTGCGTCCGGTCCGGCTCAGC  
CCCTGGAATCCCATGACGTATCTGCGCAACGACGTGCNCAACNCGTGGCTGATGTCNGTGGTGTGTTGGGGTGGGC

(SEQ ID NO. 114)

:Rv156T7.seq::

TCGCCACCGCACCGCGCGAAGCTCAAAGGCACCTACTGGCACCAAGGCCCCACAGCTCACCTGTGACCTCCTGCG  
CCGACCCCGCCGAGGTCTTGGCCGTTACCAACCGAACGGCGAGCCGGGAGTCTGTTACGCATCGAACAAGAGCAAG  
GTGCATGGGCGGAGTTGTTCCGCCACTTCGTGCGATGACGGGGTTCGATCCATTCGAGGTCCGTGCGCGCGTCCGTGCGAG  
TGGCGGTCACTCCAGGTACTCGACCTCACAGACGAGAGGACTCGATCCCATCTAGGTGTGGACGAAACAGATCTTC  
TGTCGACGACTACACCACCCAGGCCATCGCCGCGCGCCGCGATGCCAACTTCGACGCCGTACTGGCCCCGGCGG  
CGGCGCTCCCCGTTGTCAAACACTTTGCCGTGTTGCTTACGCACTGCCCAACATCGAGCCCCA (SEQ ID NO. 115)

## Clone Rv157

:Rv157SP6.seq::

ATGAAATAAGAAGACACATCCCTCAGTCGGTTATCATCACTAGCGCTCGCCGACCCCGTGTAAACCGATCATAGCGAG  
CGAACTGGCGAGGAAGCAAAGAATATCTGTTCTGTGATAGCTCTTACGCTCAGCGCAAGAAGAAATATCCCCCGCG  
GGAACAACCTCCAGGTAGAGGTACACACGCGGATAGCCAATTACAGAGTAATAAACTGTGACACTCACACCCTCATCAAT  
GATGACGAACTACACCCGATATCCGGTCACATGACGAAGGGAAAGAGAAGGATATCATCTGTGACAACTGCCCTCA  
AATTTGGCTTCCTTAA (SEQ ID NO. 116)

## Clone Rv159

:Rv159SP6.seq::

ATACTCAAGCTTGTGCAACTCCTTCTGAATACCGGCCCGCCATCCACAGATGCCCGGAAGAACTTCCAGGTACCCAT  
GGCGGCTGGATCAGGGGGCGGCACAGTTGGTCTTGTCTCGCTCGAGTGGCGTCTGTTGTCGGCTTGGACGGGGCTCC  
GACGGTACCGGAGGGCAGCGACAAACACTTATGCACTTGGGCGACCCGCCGAGACGGTGGCAGACCCATCCCGACGG  
CACAAGCTCAGCCGCGCGGCTCTTGTCTTCGTGCGATCGACATTCACCCACTTCTGACCGGGCTTGGGCGAAGGAA  
GCAGAA (SEQ ID NO. 117)

:Rv159T7.seq::

GGTATAGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTCGGCGGCTACGTGCCATCGAGACACTGGCGCA  
GGCTATCGCACCCGTTATCGGCTACGAGCAAATCGCGGTATGCGTTCTTGAGCATGAGTCGGCGACCGTCTGTCATGGT  
CGACACCCACGACGGAAGACGAGATCGCCGTCAAGCATGTGTGCCGCGGATTATCAGGACTGACCTCCTGGCTGAC  
CGGCATGTTTGGTGGCGATGCTTGGCGCCCGCGGCGTGGTCTGCTGGTCCGGTCCGATAGCGAGGTACGCGAATTCTC  
GTGGCAGCTCGAAAGGGTCCTGCCGTGCCGGTCTTTGCGCAAACGATGGCGCAGGTTACGGTTCGCGCGGGGTGCGGC  
CCTGGCGGCGGCCA (SEQ ID NO. 118)

## Clone Rv15

:Rv15SP6D2.seq::

GACACTATATNATACTCAAGCTTCAGGTCAATGTGCGCCAAGCCCTGACGCTGGCCGACCAGGCCACCGCCGCCGGAN  
CCCTNTCTAGA (SEQ ID NO. 119)

:Rv15T7.seq::

CTGTAGCCACCTGTTGCCATCCCCGTATGCCGACTCTGGTCTATCTCGGATCCGCTGACACCCCGCTAAGGCTGCTC  
CTCTCGGTGCATTACCTCACCGACGGCGAACNCCCCAGCTTTACGACTATCCGGATGACGGCACCTGGTTGCCGGCT  
AACTTCACCGTCAGCTTGGACGGCGGCGTACCGTGCATGGCGCCAGCGGGCGATGGCCGGGGCCGCGACCGATTC  
GTCNTCANCCTGTGCGGTGAACCTGCCGACGTATCGTGGTGGTGTGGGCACCGTGGCGATTGAGGGCTACTCCGGC  
GTCGGATGGGTGTGTCAGCGCCCGCACCGGCGAGGCCGA (SEQ ID NO. 120)

## Clone Rv160

.....Rv160SP6.seq:.....  
ATACTCAAGCTTCGCACGCTCGGCGCGCGCGGTACCGCCAGGTCGCCAACAGATCGTCGATGTTGCGCTCGTCCGC  
CTCGCGCAGTGGTCTGTCAACAGTCAACGTTAACGCCGCCGACATGTCCTGCGGCGGGCAAAAACGTGAAAAACG  
AGCGGGCGACTGCNATGTATGACACCGACGGCCCGCATGGGCCAGGGTCTGGCAAATTCGATCTGTGCGGCCAGT  
GCCAGCAGCGTCGCCTCGTCATACGGCCGGCCGACGAGTTGAACCGACATGGGCAGGCCGTGCGCGTCGAAGTCCAC  
GGCACCACGGGCGCGGGCTGGCCGTCAGATTCCAAAATTGAAAGTACGGAACCGCTGCACCACAA (SEQ ID NO. 121)

## .....Rv160T7.seq:.....

ATCGTTTCGACCAGGCGCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCAGGTGCCACCACGCTGGTCACTGCG  
CGTTCAGCTCGCTTGCGGCGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTGGCGCAGCTTGGGGATCGCGACGTCG  
ATGGTTGCGGCGACGGGTGTCAAATCACGGTGGCGGTAGCCGTTGCGCTGATTGGACCGCTCATCGCTGCGTTGCGGG  
TAGCCCCGCCCCGACAGGGCGTCGGCTTCAGCCCCCATCAAGGCGGCGATGAACGTCGAGAGCAGCCCGCGCAGCAGA  
TCCGGGCTCGCCTGTGCGAGTTGGTTCAGCCAGAAGCTGCTCGGTGTCGATAAGATGANAAGAAGTCATTGCGTTATTT  
CCT (SEQ ID NO. 122)

## Clone Rv161

.....Rv161SP6.seq:.....

ATACTCAAGCTTGGGTGTGCCGATCACCGGAAGCCGCGATGATCAGCCACGTTTCGCGCGCGCCCGGCATAGGGCGGGC  
TACCGATCTCCGCGTCATACACCCGCGGGTAATCGCCGACGGTGCCGGTTGCGGAGCCGAAGGTGACGACGCTGATTG  
AATCGAGTTCCAGGTCCAGCGGGTGGCGCAGCAACGGCGCGAGCTCAACNACGTCATACGTTGTGCTTTTCTACGG  
TCACCGACCCGGTGACCGTAGTCGCCCCGGTGCGCTCGGCCGAGAAGTTGCACCGCCACCACCGCGACAACGTCCTGCA  
CGCGGACGCCACCCCGGAT (SEQ ID NO. 123)

## .....Rv161T7.seq:.....

GCGCNAACAGCTCGCGGCGAGCCACGACGTGCTGCGTCGGATTGCCGGCGGCGAGATCAATTCCAGGCAGCTCCCGGA  
CAATGCGGCTCTGCTGGCCCGCAACGAAGGACTCGAGGTACCCCCGGTGCCCGGGGTCGTGGTGCACCTGCCGATCGC  
ACAGGTTGGCCCAACCGGCCGCTTGATGCCCGGTGCGCAAGCCCGGAGTTGCCAAACCCAGCGTGATCAGGCTCG  
GCTCGCGAGTTGCGCGAAAAAGTGGCTCGCCTGATCACCTACCATCGGCCAGGATCTGCGTGTGTCATCAGCAGCTCGC  
CAAGGAGGTTGTTGTGGTGTATCGACGGCCTTTAGCCAGATGTTTCGGAATCGACTATCCGATAGTGTCCGCGCCAAT  
GGACTTGATCGCCGGCGGTGAGCTGGCTGCCGCGT (SEQ ID NO. 124)

## Clone Rv162

.....Rv162SP6.seq:.....

ATACTCAAGCTTCTCCGATACCCGCCATGTCGCGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGGCGGGAT  
CCCAAAGTGCGGATGATCGGGCCGCTACGTCGTGGTGTACCTCGTCGGTAACAACGAAACCGAAGCGTATGACTCGG  
TCCACGCGGTGCGGCACATGGTGGACACCACCCGCCACCGGCGAGGGTGAAGGCCTATGTACCCGGTCCGGCAGCAC  
TCAATGCCGACCGAGCCGAGGCCGGAACAAAAGTATCGCTAAGGTCACCGCGATCACGAACATGGTGATCGCAGCAA  
TGTTGCTAGTGATCTATCGCTCCG (SEQ ID NO. 125)

## .....Rv162T7.seq:.....

CCATGAGCACCGCCAGCCGAGCAGAGGCCAACTCCGCCGACGAGGCCGGTTGGACTTGTGCTGCTGGACAAGGGG  
TTTAGCCGCCGAAGCAGTGACGTACATCGGCGAAGAGCAGTTGCGCTGTCGACCGACGGCGCAAACCGTGAGGCTAGG  
GAAGCGAGGAGCATGGCCGCCGACCCGCAATGTACACGCTGCAAGCAAACCATCGAACC CGGATGGCTATACATCA  
CCGCCATCGCCGCGGTCAAGCCGGGATCGTCGATGACGGCGCAGTACTGATTCAGTGCCCGGTGAATGCCGCACCC  
CGGGGAGCACTTCCGCCAAACTAACC CGTTGG (SEQ ID NO. 126)

## Clone Rv163

.....Rv163SP6.seq:.....

CGGGTGTCATTGGCCACCGCGCGCGCTGTCCGGGAAATGGCGGGTCCCGGTGGTTTTGCTGAGGAGTGCTGAACCG  
TAGTCGAAGTGGGCGGCGTCAGACTCCACCAGCCAGCAGGCAGCGCAANCTGAATCCTCCAACCGGGTTGTCNATC  
CGGACAGGTTGGGGTGCCTTTGGGGCAATNACAGGTGGCGGCGGTGCGTTCGGGTGCGCCGGCGGAGGTGCTGCNTTG  
GGATCCCCGGCTGGGCATTGCGCNTGTTGGCGGCGGCCGGTGGTGGGGGGGCAACACGTGTCNCCGGTGCGGGTGGC  
CCT (SEQ ID NO. 127)

## .....Rv163T7.seq:.....

CCAAGATCTACACCATCGAATACGACGGCGTCGCCGACTTTCCGCCGTACCCGCTCAACTTTGTGTCGACCCCTCAACG  
CCATTGCCGGCACCTACTACGTGCACTCCAATACTTATCCTGACGCCGGAACAANTTGACGCAGCGGTTCCGCTGA



CCAATACGGTCGGTCCACGATGACCCAGTACTACATCATTGCGACGGAGAACCTGCCGCTGCTAGAGCCACTGCGAT  
CGGTGCCGATCGTGGGGANACCCACTGGCGAACCTGGGTTCAACCAAACCTGAAGGTGATTGTTAACCTGGGCTACGG  
CGACCCGGCCTATGGTTATTGACCTCGCCGCCCAAATGTTG (SEQ ID NO. 128)

## Clone Rv164

.....Rv164SP6.seq:.....  
AGCTTCCCAGATTCCGGCTTTGGATCAAGACCCAGTCCGCGGGCGCGATCCGGCNGCTCGGTGACTACATCAAGCCAC  
AAATCGACGGCTTTCCGGGTGCCGATACCGATGACGTGGCGGATGTCGAGTGTTGAGTTCTCGGCGGGCGGATGCTC  
ACCTGGCGATCACCTGCCTCTCGTTGACGATCGATCGTCTATGCCGCCGTCTCTGCGGGAACAGGCCNCCAGTACATC  
GCCACAGACGGGATCCACCCGATTTCCGGCTACGGTTGCTCGTTCCGGTGTTCCGACTAGTCGGTCCCTGGTGACGTGC  
CGGTGATGCGGACCGGTCTAGCACTGACCAATGGCCAAATGCGGGC (SEQ ID NO. 129)

.....Rv164T7.seq:.....  
CGGGGGGCTCTTAATAGTGTAGGAAAGAAGCTCTACATATTCAAGAGGATTACCATGGCTCGTGCGGTCCGGGATCG  
ACCTCGGGACCACCAACTCCGTCTCGTTCTGGAAGGTGGCGACCCGGTCTGTCGCCAACTCCGAGGGCTCCA  
GGACCACCCCGTCAATTGTCGCGTTCCGCCGCAACGGTGAGGTGCTGGTCTGCCAGCCCGCCAAGAACCAGGCAGTGA  
CCAACGTGATCGCACCGTCCGCTCGGTCAAGCGACACATGGGCAGCGACTGGTCCATAGAGATTGACGGCAAGAAAT  
ACACCGCGCCGGAGATCAGCGCCCGCATTTCTGATGAAGCTGAAGCGCGACGCCGAGGCCTACCTCGGTGAGGACATTA  
CCGACGCGGTTATCACGACGCGCCGCTACTTCAATGACGCGCCAGCGTCAGGCCACCAAGGACCCGGCCAGATCGCCGG  
TCTCACGTGCTGCGG (SEQ ID NO. 130)

## Clone Rv165

.....Rv165SP6.seq:.....  
ATACTCAAGCTTCATAACAGGCCTGTTGTGGGCGCACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAAGTGCGGCC  
CGCACCGCCGGCATCTCCGGTCACGCAGGGCCGCGGCCCGCGCCGAGCGACGGCGTGTTCGCGCAGTTTCGCCGTCA  
ATGATGCTGACCTGATCGGCCACCCGGGCGTTCTCGGCGTCTTCGCGTTCACTAATCGCGGTGCTCAGCAGCGTCTCG  
ACAGCCACCAACCCGAGTGGCGACAGCTGCTCCACCACGGACCGCAGCGATGCCGTACCTCACCCGTCCAGCGGTCC  
ACCACGACACGGTCTGTCACACGCGCGGGGCATTACCAACCCAGGCGGTACCGCCAGGCCGATCGCCACACCCGCC  
ACCATCCCCGATGCAGCCAGGCCGGGAGTAAGA (SEQ ID NO. 131)

.....Rv165T7.seq:.....  
CTGGTGCTGGACGGAGCCTAGTACAACCTCCTCTCCAATGCTCTTGCCCCGATCGCGGCGACCCAGGATGACCCAGGAC  
ATCTGCGCGCCCGAAGTACTGGAAAAGCTCACACCCGAGTTCTGTCGCACCGGTGGTGCCCTACCTGTGCACCGAGGAG  
TGTGCCGACAACCCATCGGTGTACGTCTGTCAGTGGTGGTTAGGTGCAGCGAGTTGCGCTGTTTGGCAACGACGGCGCC  
AACTTCGACAAACCGCCGTCNGTACAAGATGTTGCGGCGCGGTGGGCCGAGATCNCCTGATCTGTCCGGTGCGAAAATT  
GCTGGATTCAAGTTGTAGAACTAAAT (SEQ ID NO. 132)

## Clone Rv166

.....Rv166SP6.seq:.....  
ATACTCAAGCTTTTCCGGCGTCTGTCACCTGACCCAAAAAGCGCAGGTGCGCCGCCAAACGGCCCCGCTGGCCGCGCA  
ACTGGTCCGGCTCGCCGTGGCCGACAATCAGTAGCTGGACATCCGGAACCGCTGCACCACTTCCGGCAGCGCGTCAA  
GCAAAAACGGCCATTCC (SEQ ID NO. 133)

.....Rv166T7.seq:.....  
TTTCAGATCTCATTTTTATGACATGACTGGAGATCTGTCTAGATTGCAGCTCCTGTGAGCGTGGGTACCGGATTCAAG  
CCGGTCCGGTCACGCCGCGGTGGTACCGGCTTTGCGGCAGTGCTCGGCCTCGAGTTCGGCGATCGCGCGCGAAGTGCGT  
TTCGCGCACCAAGATCGCGGCCTAATGGCCGCGGATGACCCGCGATGACCAGCGCGATCCAGGAAAAACCGTTCCAACC  
AGTGCTGGGCGGCCATCCCCG (SEQ ID NO. 134)

## Clone Rv167

.....Rv167SP6.seq:.....  
ATACTCAAGCTTCCCGACCAAGTTGAACAGCACCGATTTCGGCGAGCACTTCGTCAACTTCCAGGGTGCCCGCACC  
AAGTATTTGACAAAGTATTTCCGTCCGGGCCCGCCGCCGCGCGCGGAGGTGGTCATCTTGGCGGCGGGGCTGGAC  
TCCCGCGCGTACCGGCTGCCTTGGCCCGACGGGACCACGGTTTTTGAAGTGGACCGCCCGCAGGTCTTTGATTTCAAG  
CGCGAGGTGCTCGCCAGCCACGGTGCCCAACCGCGCGCCCTGCGCCCGCA (SEQ ID NO. 135)

.....Rv167T7.seq:.....  
GTGTGCTGTCAATTCAAGCTGAGCCTGATGCACTCAACTTACTGAGCATGCTAACGCTGGTCTGCGGGTCTTGTTTC  
CCGCTGTGCGGCAGGGCACACGCTCGGGCGTAGCTGGGAGAGGCCCGGTCAAGCCCGGAGAGCAGTGCTCAGTCCG

CCAGCTTGACCGACTTTTCGATGAGAACGCGCTTCTCGCCGTATTGAACTGGCGTGCTGACGGTGCCTGAGCAGCGCTC  
GCCGAGTGCGGCCGCTGATTCTTTCATCGAGCCAGGAGGCGCATTTCGTGTTTCGGCCGCTGCGGGTCGGCCCCATCGT  
CGACGCGATCCGTCACCCACTCCTCGATCAGGTCTGCCTCATCGAACGGGCCAACGGTGTGTGCGGAGTATGTGTGCG  
TGGGCACGGCGAGCCGGGTGCTGTGGTACACCCACCGTTGCATGACCAAGTTGACGCCTGACTGGCTGAGCACC GCGA  
TCCGCTCACAGGTCGGAACGTTGGTG (SEQ ID NO. 136)

## Clone Rv169

.....Rv169SP6.seq.....  
ATACTCAAGCTTTTGGTCTAGCCGGCCGAGCCGATACAGGTGTCATTGGCCACCGGCGGCGGTGTCCGGGAAATGG  
CGGGTCCCCGGTGGTTTGTCTGAGGAGTGCTGAACCGTATGCGAAGTGGGCGGCGTCAGACTCCACCCAGCCAGCAGG  
CAGCGCGAACTGAATCCTCAACCGGTTGTGATCCGGACAGGTTGGGGTGCCTTTGGGGCAATGACAGGTGGCGG  
CGGTGCGTCCGGGTGCGCCGGCGGAAGTGTGCGTTGGGATCGCCCGGTGGGCATTCTGCGTGTGGCGGCGGCGG  
TGGTGGGGGGGCAACAGGTGTCTCCGGTGCGGGTGGCGCTGCACC (SEQ ID NO. 137)

.....Rv169T7.seq.....  
GGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCCGCGACTTTCCGCGGTAC  
CCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTTTCATCCTGACGCCG  
GAACAAATTGACGCGAGCGGTTCCGCTGACCAATACGGTCCGTCACGATGACCCAGTACTACATCATTGCGACGGAG  
AACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAACCAAATTTG  
AAGGTGATTGTTAACTGGGCTACGGCGACCCGGCTATGGTTATTGACCTCGCCGCCCAATGTTGCGACTCCGTTG  
GGGTTGTTCCAGAGGTGAGCCCGGTGCTCATCGCCGACGCTCTCGTCGCCGGGACCCAGCACGGAAT

(SEQ ID NO. 138)

## Clone Rv16

.....Rv16SP6.seq.....  
TTCTNTCTTCCNNATTCTGNNNTCTNTACTACNNGGGCCNCAAAACACCTTGGCNAACGCTCAAAGGCGNTACNGG  
CACCAAGGCCCCACACGTCACCTGTGACCTCCTGCGCCGACCCCGCCGAGGTCTTGGCCGTTACCCTGAACGGGC  
GAGCCGGGAGTCTGGTACGCATCGAACAAAGAGCAAGGTGCTAGGGCGGAGTTGTTCCGCCNCTTTTTTATGACGGG  
GTCGATCCATTGAGGTCCGTGCGCCGCTCGGTGAGTGGCGGTCACTCCAGGTACTCGACCTCNCAGACGAGAGG  
ACTCGATCCATCTANGTGTGGACNAAACAGATCTTCTGTCCGACGACTACACACCCAGGCCATCGCCGCCGCC  
GCGATGCCAACTTCNACNCCGTNCTGGCCCCGGCGGGCGGCTCCCCGGTTGTCAAACACCTGCCGTGTTGTTACN  
CACTGCCCAACATCNAGCCCGANCNATCCNAGGTCCGTCCAACGCCCTCCGCGGCTCNCCAACCTNCTCCNCTGATCN  
TCCGCACCAACACATGCCCGACTCCNTGCNCCNATTGCTTGNATCCCT (SEQ ID NO. 139)

.....Rv16T7.seq.....  
CCGCTATCGGTCCGTGTGCTTGGCGGCGTCCGTATCAACACCGCCACGAAATGGGGCACAAGAAGGATTGCTGGAG  
CGGTGGCTGTCAAAGATCACCTCGCCAGACCTGCTACGGGCACTTCTACATCGAGCACAACCGTGGCCATCACGTC  
CGGGTGTCCACACCGGAGGCCGCGTCCGCGCGGTTCCGGCAGACGTTGTGGGAGTTCTGCCCGCAGTGTATC  
GGCGGCTTGGCTCGGCCGTTCAATTTGGAGGCCAACGGTGCCTCGGCTCGGCGTCAGCCCTGGAATCCCATGACG  
TATCTGCGCAACGACGTGCTCAACGCGTGGCTGATGTGCGTGGTGTGTGGGGTGGGCTGATCGCGGTCTTCGGCCCG  
GCGCTGATCCCGTTGCTCATCATCCAGGCAGTCTTCGGCTTCAG (SEQ ID NO. 140)

## Clone Rv170

.....Rv170SP6.seq.....  
ATACTCATGCTTGCCGAAGTCCGATGGGTGCGCGCGGCCANCCAGCGAAGTCGCTAGCGTGGCCGTGTTCTTGGCT  
TCGGATCTATCCTCGTACATGACCGGCACCGTGTGGAGCTGACTGGCGGCCGTTTCATATGACACCGAGATCATTGC  
CACGGTACGGCAATTCGTCAAGAAGGAAATCTTCCCAATGCACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGA  
AATCGTGCATCGGCTGGGTGTTATTGGCTTGTGCGGTGCGCGGCTGCAAGGGTATCGACACCACCGAGTTCATTCTCC  
GGGCGTGCC (SEQ ID NO. 141)

.....Rv170T7.seq.....  
GGCGTCAACGGTGTGCGCACCGGCTCCTGCAGTTGGTAGGCCTGCAGTTTGTGCATCAGGCCGATGCCGCGGCCCTC  
GTGGCCACGCATGTACAGCACCGCGCGGCCCTCACGGGCGACCATCGCCAGCGCGGCGTCCAGCTGAGGCCCGCA  
ATCGCAGCGGCGTGACCCAAACACATCGCCGGTCAAGCACTCCGAATGCACCCGGACAGCACGTCGTCAACGTCGGC  
GTTGGGCCCGGCGATCTCGCCGCGGACAGCGCGACATGTTCCAGTCTCTGATAGTGTGGTGTAGCCGATGGCGCG  
AATCTCCCATGACGAGTCGGAATCCGCGCCTCGGCG (SEQ ID NO. 142)

## Clone Rv171

.....Rv171SP6.seq.....  
ATACTCAAGCTTCGGCCTCGCTGCAGGAGTGGGAGCCGACGGGCTGGAAATCCGAAAAACGAGCCGGTGATCGCACTG  
TCGCCGATCGGGGCCGACCTGGTTGGTGTACCGATGAATCCGCACCCAAAATGTGGCTGCGGTGGCGTTTCTTGAC  
TCCTTGCGCTCGACTCTTGTGGCAGCCACCGAGCGGTTGGTCCAGGATCTGGATGGGCAAAGTTGTGCGGCCCGGCCG  
GTGACGGCCGATGAGCTGACCGAGGTCGACAGCGCCGTGTTGGCTGACTTGAACCGACATGGATTGCCCCGGTTGG  
CGTCACCTCAAGCATTTCAATGGTTAT (SEQ ID NO. 143)

.....Rv171T7.seq.....

ATGCGTCACCCCGATGCGCCAGATCGGGGCTTCGCAAATAAAGCACGAACAGGCGGGCAAACGTCTATCTCGGAGC  
CGGAAGGGCAATCAGCCGACCGTCGACGAACGACACCGGCGATAACCACTTAGGCGTTGAACGGCCGGCCAAACATT  
ACGCCTCCGTTGATAAGGCTTTCGGTCTCTTCCCGGTATCCCAAGCACCTTGCGGCAAATTTGAACGCTTTCCTGT  
CCGGGCACCGGCCCGGGCTTGGGGTCCNTCCGA (SEQ ID NO. 144)

## Clone Rv172

.....Rv172SP6.seq.....  
ATACTCAAGCTTCAATCGCGCCGCCACAATCCAAATATGCGTCTAGCGTCTCGATGAGCGTCGGTCCGGCATCGGCTA  
GGGGCCGCATCACGTCGGTATGACGGGCCACGATCGCCCAAGGCGTCGCCCATCAAGGGCGCGTTCGGGCAAAAATTC  
CCCTATCCAGCACGGGCCGCGGCTCCGCNCCAGCCGGCGACGGCGTTCATCCCGAGATCGCCTCGCTAGCGCTGC  
GGTGCGCCGCGGTGAGCATGGGCGCCGTGGGGCCGATGACCACCGGGGCGT (SEQ ID NO. 145)

.....Rv172T7.seq.....

TTGCGCGGGTCTGTAGATTGCGGTGCGGCCACCCACAGGCACTCATGAACCGCAGCCACGATCGATCTCGGTGG  
(SEQ ID NO. 146)

## Clone Rv173

.....Rv173SP6.seq.....

GCGCACCATCGCCAGTAGGTGCCCCGTGGTGGGCGCGTCGAGCCACCCGAGCGGAAACGCGAGTCCGAACAGCAACAG  
CAGGACGGGCGCAACCAGGGCGGTGACCATGCCCCGGCGCTGAACATCAACCACAGGAAGGGCTCCGCCGAGCGTCC  
GCGCGACC (SEQ ID NO. 147)

.....Rv173T7.seq.....

CATCGTCGAATTCGGTCCGGGTTGNTAGNACCGCAGCACCAAACGCACCCACCGACCCCCACGCTTCACGCCAACCC  
TTTAGTTTCATTGGCGTGAACAGCAGCGTAGCCGTTGCCCGATATATGTGGAAAAATCGTTCGGACGTACAAAAAA  
GTTCTGACGCTGGCGTCAACTCGAAACTGCCTCGGAAGTCAATGATGATCCATCAGTCAATATTAAAGTCG  
(SEQ ID NO. 148)

## Clone Rv174

.....Rv174SP6.seq.....

ATACTCAAGCTTGTCTGCTGCCTCAGCGTATGCATCCAACAGCGCATCGCGATCAACGATCAGGCGCGCCGATTTCCG  
GCCGCGGGCAGTGGCACTGGCCAGATGGCCGTTTTTTTCGAGAACTTCAACGCCTGAGCGCTGCTTCCCATCGAGAG  
ACCGGTGGCCTCTACAACCGATGCGACAGTTGGACCGCGCATGTTGCCAGCAGCGCTTCACATACGGCAAGTNTGGC  
GCGG (SEQ ID NO. 149)

.....Rv174T7.seq.....

TTGTCCAGGCGGGGAATCGGGCAGGGAGACGACACCTTCGTTCCGTTTCGATCGTCGGAACGGGTAGTTGGCCGCGAC  
CACGTTGTTTCGGGTGAGCGCGTTGAAAAGTTCGACTTGCCGACGTTGGGCAGGCCACGATCCCCAGGCTCAAGCT  
CACAGA (SEQ ID NO. 150)

## Clone Rv175

.....Rv175SP6.seq.....

ATACTCATGCTTGGCGCCTGGGTGGCAGCCACCTGCCACACAGGACCGCGGTGCGGACGCGGCTGACGCGCCTG  
GTGGTCAGCATCGTGGCCGGTCTGCTGTTGATGCCAACTTCCCGCCGCGCAACTGCTGGTGGGCGCGGTTGGTGGC  
CTCGCATTGCTGGCCTGGGTGCTGACCCNCCGCNACAAACACCGGTGGGTGGGCTGGGCTACGGCCTGCTATTCCGC  
CTGGTGTCTACGCTCTCGTTGTTGCCGTGGATCGGCGAGCTGGTGGGCCCCGGGCCCTGGTTGGCACTGGCGACGACG  
TNCGCGCTGTTCCCCGGCATCTTCGGTCTGTTGCCGCTCGTGGTACCCTGTTGCCGGGTGGGCC (SEQ ID NO. 151)

.....Rv175T7.seq.....

CGCCAATTACGATATCGTTAACCGATATCCCGAGCCGATAGCTGGCGGGCTCGGGTGGTGGCCAGCGGCGCTGCGAC  
GAAAGGTGTGACCGTCATGAAACAGACACCACCGGCGGCCGTGGCCGCTCGTACCTGCTCGAGATCTCAGCATCCGC

AGCCGGTGTGATCGCGCTTTCGGCGTGTAGTGGGTGCGCGCCCGACCCCGGCAAAGGCCGGCCCGACACAACCCCGGA  
ACAGGAAGTCCCAGGTACCGCGCCCGAAGNACTTGATGCGCGAACNCGGAGTGCTCCAAACGCATCCTGCTGAT

(SEQ ID NO. 152)

Clone Rv176

.....Rv176SP6.seq:.....  
ATACTCAAGCTTGGGCACTGACTTCGGTACCCCTCCGCTTTGGCCAGCAGCAGCCACAGCGCGGTTTCGCGGACCGA  
ACGTGGACATCAATAGCCCGGAATCGGTGTGTGCAAGTTGGTAAACGGTGTGATCCCAAGCTTTGCCAGCCTTTTCG  
TAGTCTTGGGCCCCACACCCACAGTGCTTCGACGGTACGGTCACCCATGATGGCCATCCAGTTGGCATCGGTGAGCT  
GATAAATGCCAGCTGGTTTCGCCAACCCGGTAGCGATCTTGGCGCGCTGCTTGTGTCACTGATACCTATCGAGCAAG  
ACAGCCCGGTTTGCAGACAAATGACTTTTCGGATCTCTTCGGCGACTTCGATGGGGTTCGTCGGGA (SEQ ID NO. 153)

.....Rv176T7.seq:.....  
AAAGTCTGTGCCGGTTCGCTAAACACCCGGCGGACACTCAGACGGTGTGGTGGTGCGGCATGGCACCGCGGGCAGC  
AAAGCGCACTTCTCCGGGGGACGACAGCAAGCGACCGCTAGACAAGAGGGGTGCTGCGCAGGCAGAAACGTTGGTACA  
CAGCTGCTGGCGTTTCGGCGCCACCGATGTTTATGCGCCGACCCGGGTGCGCTGCCACCAGACGATGGAGCCACTCGCC  
GCGGAATGAACGTGACCATAACA (SEQ ID NO. 154)

Clone Rv177

.....Rv177SP6.seq:.....  
ATACTCAAGCTTGGGTTCCACGCCCCGCGCAGCCACGCCGTACCTTTCCACGAGACCTCACCTGCCGATCCGAAATGG  
AATCGGCCGTGACGGAATTGGCGCACCGAACACCCAACGAGGTGGTGGCTTCGTGCGGAACCGTCACCCGAGTCGCGG  
CCACCGTGCGCACGGCGACGTTCTACACCCGCACCAAGATCCGAAAGCTGCAAGCTCCCAGCACCGATCCCGACGTCA  
TCACCGCTGCCGCGGCACGTCTTGACCTATTGAGCTGGATCGGCCGTCCGGTTGCTGGGAGTGCGGTTAGAAC  
TGGCCTAGAACCGGCGGCACACCCGNCCTGGGCGGGGCGAATTCTTGACCGCNCGGCC (SEQ ID NO. 155)

.....Rv177T7.seq:.....  
CGCGGTTGGCGTAGTTGGACGGGTGCGCCTCCGAGGCCAATGATGACGATGACCACGCCGATCACGATGGCCACCGAG  
AGGGACAACAACAGAAAGCTGACGAATCCCTCCTTGGCGGGCGGGCTTTGTGGTGCCTGGTCCGATGGGCGCGAAT  
TTACGGCCCCGTCCCCCAGGCCCGCGAAGCAGGGTCCCCAGCCAGTTGGCGTAGGCGGAATTAACGATCAGCGCCA  
CCGCGATAACCTGCCATGCCTCGGGCATATCGATGTGCGGCCAGAACAGGCCGAAC (SEQ ID NO. 156)

Clone Rv178

.....Rv178SP6.seq:.....  
CCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGGCCAACGGTGATTTCTTGGCCGCCGCTGACGGCGCGAACG  
ACGCCAGCGACCACATTACGAGATGGCCAGCGCGTGCCGGGCCACGAGGTTGGTGCTCGGCGGCTACTCCCAGGGTG  
CGGCCGTGATCGACATCGTCACCGCCGCACCACTGCCCGGCTCGGGTTACGCGAGCCGTTGCCGCCCCGAGCGGACG  
ATCACATCGCCCGGATCGCCCTGTTTCGGGAATCCCTCGGGCCGCGCTGGCGGGCTGATGAGCGCCCTGACCCCTCAAT  
TCGGGTCCAAGACCATCANCTCTGCAACAACGGCGACCCGATTTGTTGACGCGCAACCGGTGGCGAGCGCACCTAG  
GCTACGTGCCCGGGATGACCAACCAGGCGGCGCGTTTCGTGCGGAGCAGGATCTAACCAGGAGCGCCCATAGATTCC  
CG (SEQ ID NO. 157)

.....Rv178T7.seq:.....  
TAANACCCGTGTAATTTGGGATGGGCAAAAAGGCCAAGCACCGCGTGCCACGAACGCCGGGAGGGACAATCTCGGGC  
GGCTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGCTCNCCTCCGACCGCGAACATTTCGG  
GGATGGCAGCAACCTGGTAGCNCCTGGCCGGGCGATGATCTGCAGCGTCGCCGCGGGTAGTCGCCGCCCCGGGCGGCT  
ACAGTCTGAAACGCGATGACCATCGATGTGTGGATGCAGCATCCGACGCAACGGTTCTTACACGGCGATATGTTTCGCC  
TCGCTGCGCGGTTGGACCGGTGGGTCTATCCCGAGACCGACNTCCCGATCGAAGCGACCGTCTCTCGATGGACGCC  
GGCGGCGTCACCTGGGTTGCTCACCGCTGGCGTGGCCCCAA (SEQ ID NO. 158)

Clone Rv179

.....Rv179SP6.seq:.....  
GTCCGCAAAAGACTCAGCGGCCGACTTTGCTCGCAGCTGGCGGTACCGCGCCACCGATTTCGATGCCGTGGTTCGCGGAA  
GAATGCCTCCCGAAATCGCACGGCCGACTCCAGTTTCGGCGAGCATCCGCGATGCCAGCTGCGGCTGEGCCCTGCCGGC  
CACGGCACCCACATGCGGCGAGTTTCGTCCACCTGGGCCAGCGCCCCGCGCGGAAGTCCAAACAATAGAATGCACCCG  
GCCGATCGTGGGTAGCAGCCAACGCGATGATCAGCGTCCGACGCGGTTGACTTGCCGTTGGGGTGCACCTAC  
GACCGGACATTGCCTGCGGCCCCGGACAAGTCGATCGTCAGCGGCACCCN (SEQ ID NO. 159)

.....Rv179T7.seq.....  
CGTGGCCACGAACGCCGGGAGGGACANTCTCGGGCGGCTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCA  
ACACGTCGCGTCGCCCTCCGACCGCGAACATTGGGGGATGGCAGCAACCTGGCAGCTACCTGGCCGGGCGATGATCTG  
CAGCGTCGCCGCGGTAGTCGCCGCCCGGGCGGCTACAGTCTGAAACGCGATGACCATCGATGTGTGGATGCATCATC  
CGACGCAACGGTCTACACGGCGATATGTTNCCTCGCTGCGCCGGTGGACCGGTGGGTCTATCCC (SEQ ID NO. 160)

## Clone Rv17

.....Rv17SP6.seq.....  
ATACTCAAGCTTTGCGGCGGGCGCCGAAATGTGAACGCACCAACCCGCCCGCTGCGGGTGGCGGGGCACTCGACCT  
CGAATTTTCGCCGCCGTGACCATCCAGCCGACGGCAGTTGGGCACCCGCCCGCCCGGTGCGGGCATAACTGTTGGCGT  
CGCCGTCATAAAGCTCGAACAGCACCAGAACCGACTCCACCACCGGCCGGTGCCTCAAAATCCACGCCGATCTCCA  
CATACCGGAAAACGTGCGGTGTCCCATCGGGTTTCGGCTTGCCCGCCAGCTGCACACCACCGGTGGCCTCGGCCACCT  
TCGCGGCGCTGAGCGCAGCTACNCATCCTGACGATCATCACCCGCCCGCCCGCTCACGCTTGGCCTCCGTGACCGCAGC  
CATCGCCCGGTTGCGCGCACCGCGACGCCCGTACAGCCGCGCGCAC (SEQ ID NO. 161)

.....Rv17T7.seq.....  
AGCTTGCCGGGACTGCGGAACAGAAGCGGCGGTTCTACCGCGGTGTGCGGCCGGCGCGATATCGGCCTTTTTACTAA  
CCGAACCCGATGTGGGCTCCGATCCGGCGCGCATGGCATCGACGGCGACGCCGATCGATGACGGCCAGGCTTACGAGC  
TTGAGGGTGTGAAGTTGTGGACCACCAACGGTGTGGTAGCGGACCTGCTAGTGGTTATGGCGCGGGTACCGCGCAGTG  
AAGGGCACCGAGGGGGAATCAGCGCCTTTGTCTGAGGCTGATTGCGCCGGGATCACCGTGGAGCGGCGCAACAAGT  
TCATGGGACTGCGTGGCATCNAACGGCGTGACCCGGCTTCATCGCGTCNGGGTGCCCAAAGACAACCTTGATCGGCA  
(SEQ ID NO. 162)

## Clone Rv180

.....Rv180SP6.seq.....  
CTCAAGCTTGCGGATGCGGGCTGGCCAAACTGGCCGGGCGGGGGTTGGCTTGTTCAATCAAGGTTGGGTTGCCG  
(SEQ ID NO. 163)

.....Rv180T7.seq.....  
CCGAAGGCCCGTTCCCGGGCGTTAGCAAGCGATCGTCGGTTGGCCCACTGCGGGTGAATCTTGCGGCCGCGCCGGT  
CGTGGAACGCCAGGTCACCCGGCGGCGTACC (SEQ ID NO. 164)

## Clone Rv181

.....Rv181SP6.seq.....  
ATACTCAAGCTTTTTCTGCTCATGAAGGTTAGATGCCTGCTGCTTAAGTAATTCCTCTTTATCTGTAAAGGCTTTTT  
GAAGTGCATCACCTGACCGGGCAAATAGTTCACCGGGGTGAGAAAAAGAGCAACAACCTGATTTAGGCAATTTGGCGG  
TGTTGATACAGCGGTAATAATCTTACGTGAAATATTTCCGCATCAGCCAGCGCAGAAATATTTCCAGCAAATTCAT  
TCTGCAATCGGCTTGCAATAACGCTGACCAGTTTATAAGCACTTGTGGGCGATAATCGTTACCCAATCTGGATAATG  
CAGCCATCTGCTCATCCAGCTCGCCAACCAAGAACACGATAATCACTTTCGGTAAGTGCACGAGCTTTACGACGGC  
GACTCCCATCGCAATTTCTATGACACCAGATACTCTTCGACCGAACGCCGGTGTCTGTTGACCA (SEQ ID NO. 165)

## Clone Rv182

.....Rv182SP6.seq.....  
CTCAAGCTTGGTGCCGACATGGCCGGGCTGGAGCCCGGTATGGCAAGGTTCCGCTCAATGTGGTTGTGATGCAGCAG  
GACTACGTTGCGCTCAATCAGCTCAAACGTACCCCGTGGCGTGCTGCGCAGCATGAAGGTGGCGCCCCGACGATG  
TGGGCGAAGGCAACAGGTAACCTGGTCGGCATGGGTGAGCCCTCATTTGGGCCGTTGCGGATCGGGTTGACCCGC  
GCCGGAGTGCCGGTCAACTCAACACCGCTTACCGATCTTTTCTGCAAAATGGCGTGTGTCGGGGTATAC  
(SEQ ID NO. 166)

.....Rv182T7.seq.....  
CCGAAGCGTGGGAAATCCTGACCGAATACCGCGACGTGCTGGACACTTTGGCCGGCGAGCTGCTGGAAAAGGAGACCC  
TGCACCGACCCGAGCTGGAAAGCATCTTCGCTGACGTCTAAAAGCGGCCGCGGCTCACCATGTTGAGGACTTCGGTG  
GCCGGATCCCGTCGGACAAACCGCCATCAAGACACCCGGGGGAGATCGCGATCGAAACGCGCGGAACTTGGGCC  
(SEQ ID NO. 167)

.....Rv183SP6.seq.....  
CGACTCGACAAGCATTCTTGACAGTTGTTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCCAACAGATCATCTT  
GGTCCGGTAGCGCTCGTCCGGGTATGCTGCCGCCGGGATCTCGCTGCTATTACTCCCCCGAAAAACGCCACCGGTC  
CAGCGCGTGGCGCGCGGTCCCATCAACAACTGAACCCCAACAGGGGACATGCTTAGCGGTAGGGCGCGCGCCA  
AGGCGGCGAGCAATCGCATCACTGCGCTGCGCGTCACTATTAACCCACCCGACTTCACTTCCACGACCCGAATGGCG  
CCCGGTCAATTGATCATCTTGCGCACCGCGGATAATCCGGGATTGCCAGCCCATTCGACTACCGCATGCGAGTCATCGG  
CTGACCGCAGCGGTCCGATTACCCGAGCGCCCCGANTACATCTCTCCAATATCAATGGGCGCAA (SEQ ID NO. 168)

## Clone Rv183

:::Rv183T7.seq:::

GCGGTNTAGCTTCCCGTCGTACCGGCGACCGCCAGCCGAGAAGCTCGTTTTCCAGTGTGCTGGGGATTCTCACGCT  
GCTGCTGAGTGGTGCCAGACCGCTTCCGCTTCGGGTTACAACGAGCCGCGGGGTACGATCGTGCGACGCTGAAGTT  
GGTGTCTCCATGGACTTGGGGATGTGCCTGAACCGGTTACCTACGACTCCAAGCTGGCGCCGTCTCGTCCGCAGGT  
CGTTGCTTGCATAGCCGGGAGGCCCCGGATCCGCAATGACGGATTCCATGCCAACGCTCCGAGTTGCATGCGGATCGA  
CTACGAATTGATCACCCAGAACCATCGGGCGTATTACTGCCTGAAGTACCTGGTGCGGGTCGGATACTGCTATCCGGC  
GGTGACGACCCCCGGCAAGCCGCCATCCGTGCTGCTGT (SEQ ID NO. 169)

## Clone Rv184

:::Rv184SP6.seq:::

CTCAAGCTTGGGCGTGACGGCCACCGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGA  
CGGCGTCGCGACTTTCCGCGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCA  
CTCCAATACTTTCATCCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGAC  
CCAGTACTACATCATTCGCACGGAGAACCTGCCGCTGCTAAAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACT  
GGCGAACCTGGTTCAACCAAACCTTGAAGGTGATTGTTAACTGGGCTACGGCGACCCGGCCTATGGTTATTC

(SEQ ID NO. 170)

:::Rv184T7.seq:::

CGGGTGTCAATTGGCCACCGGCGGGCTGTCCGGGAAATGGCGGGTCCCCGGTGGTTTTGCTGAGGAGTGCTGAACCG  
TAGTCGAAGTGGGCGGGCGTCAGACTCCACCCAGCCAGCAGGCAGCGCAAGCTGAATCCTCCAACCGGGTTGTCGATC  
CGGACAGGTTGGGGTGCGTTTGGGGCAATGACAGGTGGCGGCGGTGCGTTCCGGTTCGGCCGGCGGAGGTGCTGCGTTG  
GGATCGCCCCGCTGGGCATTCCGGCGTGTGGCGCGCGCCGGTGGTGGGGGGCAACANGTGTGCGCCGGTGCGGGTGGC  
GCTGCA (SEQ ID NO. 171)

## Clone Rv185

:::Rv185SP6.seq:::

NCTTGATATTGGCGTCAACGGTGTCCGGCACC GGCGTCTCTGCAGTTGGTAGGCCTGCAGTTTGTGCATCAGGCCGATGC  
CGCGGCCCTCGTGGCCACGCATGTACAGCACACGCCGCGCCCTCACGGGCGACCATCGCCAGCGCGGCGTCCAGCT  
GAGGCCCGCAATCGCAGCGGCGTGACCCAAACACATCGCCGGTCAAGCACTCCGAATGCACCCGGACACGACGTCGT  
CACCGTCGGCGTTGGGCCCCGGCGATCTCGCCGCGGACCAGCGCGACATGTTCCACGTCCTCGTAGATGCTGGTGTAGC  
CGATGGCGCGAAACTCCCCATGACGAGTCGGAATCCGCGCCTCGGCGACCCGCTCAATGTGCTTCTCGTGCTTGGCGC  
GCCATTCGATCAAGTCAGCAATGGTGATCAGCGCCAGACCGTGCTCNTCGGCG (SEQ ID NO. 172)

:::Rv185T7.seq:::

CATAAGGGCCGGCGTACCCGGTACCGGCCGCGGGCCTACCACGTGCCGGAATGGAAGCGCAGTAAGCCCTCAACGCG  
CCACCGCTTTGGCCCGCGCGCCCGGCGTAGGCGCATCGGCGGTGGCCGTGGGGCGGCGCACTGCGACCTCACCAGCGG  
CTTTCGAGCTTTGTTTCGATCAACCGGCCAGCATGGTCGAGGATGCATTGAGACCATATTCGAAATTGGTTTCATCGG  
GGGCCCCGATCCGATGCCAGTTGCGTGAGCAAGCAGCGGAGTCTGTCGCGGGATCGATGGCCACGGGGTGT  
CAATGGCGGATGGTCCGCTGCCCGCCGACTGGCTCTTGCGGGAGAGCCGATCTAGCACCACCGATCCGCGCACGTGGA  
CCGAAACCGCGGAGTAGATGTCGAAAGCGT (SEQ ID NO. 173)

## Clone Rv186

:::Rv186SP6.seq:::

CGTCTTTTCCCCAAGATAGAAAGGCAGGAGGTGTCTTCTGCATGAATATGAAGATCTGGTACCCATCCGTGATACA  
TTGAGGCTGTTCCCTGGGGTTCGTTACCTTCCACNAGCAAAACACGTAGCCCCTTCAGAGCCNNATCCTGAGCAANAT  
GAACAGAACTGAGGTTTTGTAAACGCCACCTTTATGGGCAGCAACCCCGATCACCGGTGGAAATAGGTTCTCAGCAC  
GTCGCAATCGCGTACCAAACACATCACGCATATGATTAATTTGTTCAATTGTATAACCAACACGTTGCTCAACCCGTC  
CTCGAATTTCATATCCGGGTGCG (SEQ ID NO. 174)

## Clone Rv187

:::Rv187SP6.seq:::

CTCAAGCTTCATGTCCGTACGGCTCGGGTACGCTTCCGTCGAGTGTGCGAGTGATAAATGACGACCGGGACCTCGTC  
GGCATCTTCATAGCCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGGTAGAAGGTGCGCGAGCGCTCGGCATT  
GGTCATCGGGATATGCCGCTCGGGACGGTCAGAGCCCTCGGGTCCGGCCAGCACTCCGAGGCTTCGTCGGGGTGGTC  
CGGACACGCATGGGCCACCATCGCATTAC (SEQ ID NO. 175)

:::::::::::::Rv187T7.seq:::::::::::::  
NCGCCGCCAGCCACCACGCGCGGGTCGGGCGCGGGGCGCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACC  
GCGACACCACCCGGCTGCGCTACGTCGAGCCATACCGGGCGGAGCTACATCGGCTCGGCCGCCAGTGTTCGGGCCCT  
CTTTCGAGGTGAGGTGATACCGATTGCGCATCCGCGAGCCGACCCTGGACGACAGAACCCTGCCCTACGANTGCT  
TGTCGGGCGGGGCCAAAGAACAGCTTGGCATCCTGGCGCGATTGGCCGGCGCGGGCGCTGGTCTCCAAAGAAGACGCC  
TTCCGGTGCTGAT (SEQ ID NO. 176)

Clone Rv188  
:::::::::::::Rv188SP6.seq:::::::::::::  
CGCCACGTTTCATGGGCAACAACCCGATCACCGGTGGAAATACGTCTTCAGCACGTGCAATCGCGTACCAAACACAT  
CACGCATATGATTAATTTCGTCCAATTGTATAACCAACACGTTGCTCAACCCGTCCTCGAATTTCCATATCCGGGTGCG  
GTAGTCGCCCTGCTTTCTCGGCATCTCTGATAGCCTGAGAAGAAACCCCACTAAATCCGCTGCTTCNCCTATTCTCC  
AGCGCCGGG (SEQ ID NO. 177)

Clone Rv189  
:::::::::::::Rv189SP6.seq:::::::::::::  
ATACTCAAGCTTCAACCGATTGACGCATTGTGCGAATGACGGCGCCCGCGCATGGCCAATCCGGAAGACCATCATTG  
GCCAGTGGCCGGCGCTAACAGGTTCCAGCCCCCACCAGTCCCGCTCGAACATGCGGTGCAACCCATTTCGAGGCCG  
GCAGGGAAGACCCGCGGAAGCCGCAAGGGGCTGAGTTCCGCGCCCAATAGTGTCTCCGCAACCAGATGCGCTCGA  
AAACCGCGCCGCGAGTCAGCGCACCCGACGCGAGGTGAGAGACGTGTCAGCGCGCCACATGGGGTGCCAATCGGC  
ACGGCAGGTAGGCCGCGCGCAACCCGAACGCTGGTGCATGCCACGGTCCGCGAGGAGCGCAGCACCCGCCAATGCC  
GAAGCCACGAAACATCGGGCGCATCCACGTTCAACCTC (SEQ ID NO. 178)

Clone Rv18  
:::::::::::::Rv18T7.seq:::::::::::::  
AGCTTTTGGCAGGCTCTCCTTCGAATTCGGCGTGCACCGCTATGGGTTGCAGCAGCGGCTGGCGCCGCACACCCCACT  
GGCCCGGGTGTTCGCCCCGAACCCGGATCATGGTGAGCGAAAAGGAGATTGCGCTGTTCGATGCTGGGATTTCGCCA  
CCGCGAGGCCATCGACCGATTACTCGCCACCGGGGTGCGAGAGGTGCCGAGTCCCGCTCCGTTCGACGTCTCCGACGA  
TCCATCCGGCTTCGCGCTCGGGTGGCGGTAGCCGTCGATGAAATCGCTGCCGGCCGCTACCAAGGTGATTCTGTC  
CCGTTGTGTCGAAGTGCCTTTTCGCGATCGACTTTCCGTTGACCTACCGGTGGGGCGTCGGGCACAACACCCCGGTGAG  
GTCGTTTTTGTGAGTTGGGCGGAATCCGTGCTCTGGGTTACAGCCGAATCGTCAC (SEQ ID NO. 179)

Clone Rv190  
:::::::::::::Rv190SP6.seq:::::::::::::  
ATACTCAAGCTTTGTACACCAACTGTTTCACACGAGCGCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCAGGT  
CGCCACCACGCTGGTCAGTGCAGCTTACGTCGCTTGGCGCGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTGGCG  
CAGCTTGGGGATCGCGACTTCTATGGTTGCGGCACGGGTGTGAAATCACGGTGGCGGTAGCCGTTGCGCTGATTGGA  
CCGCTCATCGCTGCGTTTCGCGGTAGCCCGCCCCGACAGGGCGTCCGCTTCAGCCCCCATCAAGGCGGCGATGAACGT  
CGAGAGCAGCCCGCGCAGCAGATCCGGGCTCGCTGTGCGAGTTGGTCAGCCAGAACCTGCTCGGTGT (SEQ ID NO. 180)

:::::::::::::Rv190T7.seq:::::::::::::  
CCTTAAGCCCCGAGGGCCCGGCACGCGCGGTACCGCCAGGTGCCCCAACAGATCGTCGATGTTTCGCTCGTCCGCC  
TCGCGCACGTGGTCTGTACCAAGTCAACGTTAACGCCCGCCGACATGTCCTGCGGCCGGGCAAAAACGTGAAAAACGA  
GCGGGCGACTGCAATGTATGACACCGACGGCCCGCATGGGCCAGGGTCTGGCAGATTGATCTGTGCGGCCAGTG  
CCAGCAGCGTCGCTCGTCATACGGCCGGCCGACGAGTTGAACCGACATGGGCAGGCCGTCGCCGTGCAAGTCCACG  
GCACCACGGCCGCGGGTGGCCGGTCAGATTCCAGACTTGAAAGTACGGAACCCGCTGCACCACAGCAGCAAGCTCG  
AAACTGCACCCCGCGTTGGTAGGCGCGATGCGGGACGGGCCGTCGCGCGCCCTGGCGTCACAACCTAGTTCGACAT  
CGTCGAAGATCGACTGGATCGGCTGCTCACACCACTCGGCGGCCGCGAGCCGCCATCCGCGCTC (SEQ ID NO. 181)

Clone Rv191  
:::::::::::::Rv191SP6.seq:::::::::::::  
AGCTTTTTCGAGCGTCGCGCGGGGCGAGCTTCGCCGGCAATTCTACTAGCGAGAAGTCTGGCCCGATACGGATCTGACCG  
AAGTCGTCGCGTGCAGCCACCTCATTGGCGATGGCGCCGACGATGGCGCTGGACCGATCTTGTGCGCTTGGCG  
ACGGCGACGCGGTGGTGGTCAAGTCCGGTCTACGCTTGGGCTTTGCGGACGGTCCCGACGCTGGTCGCGGTTGCGC  
CGCGAAAGCGGGCGGGTGGGTGCCATCAGGAATGCCTACCGCCGCGGCACTGCACGGCCAGTGCCGCGCGGATGTCA  
GCCATCGGGACATCATGCTCGCTTCATACTCTCGACAGTCCGCGGAACAGCTCGATTCCCGGACCGCCAGCGCA

TTGGTGATGGAATCGGGCGAACTTGGCCACCCGCTGGGTGTTGACATCCTCGACGGTGGGCAATTGCCCCCGGTAACGT  
TTGCCGCCT. (SEQ ID NO. 182)

.....:Rv191T7.seq:.....  
CGGTCCGACCCTGTTTCGACGGCTACCTGAATCAACCCGATGCCACCGCCGCGGGCTTCGACGCCGACAGCTGGTACCG  
CACCGGCGACGTGCGGGTGGTCGACGGCAGTGGGATGCACCGCATCGTGGGACGCGAGTCGGTTCGACTTGATCAAGTC  
GGGTGGATAACCGGGTCGGCGCCGGTGAATTTGAAACGGTGCTGCTCGGGCATCCGGACGTGGCGGAGGCGGCAGTCGT  
CGGGGTGCCCCGACGATGATCTAGGCCAGCGGATCGTTGCCTACGTAGTCGGCTCAGCGAATGTCGATGCGGACGGGCT  
TATCAACTTTGTTGCCCAACAACTTTCGGTGCACAAGCGCCGCGCGAGGTGCGTATCGTANATGCGCTGCCGCGCAA  
CGCTTGGGGAAAGTGCTCCAGAACATTGCTGTGAGAAGCTGANCTACGCGAATTATCGTGTTACGCTGGA

(SEQ ID NO. 183)

Clone Rv192

.....:Rv192SP6.seq:.....  
ATACTCAAGCTTGCCGAAGTTCCGATGGGTGCGCGCGGAGCCAGCGAAGTCGCTACCGTGGCCGTGTTCTTGGCT  
TCGGATCTATCCTCGTTTCATGACCGGCACCGTGTGGACGTGACTGGCGGCGGTCCATATGACACGGAGATCATTGC  
CACGGTACGGCAATTCGTCAAGAAGGAAATCTTTCCCAATGCACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGA  
AATCGTCGATCGGCTGGGTGTATTGGCTTGCTCGGTGCGCGGCTGCAAGGGTATCGACACCACCGAGTTCATTCTCG  
GGCGTGCCGGCGCATTGAGCTGGCGGTGCGCGCTGCCAGCACCGTCATAGGTACTTGACGATGGTCCACGTGCGAC  
GAGCGCCTCCACGTGCTGCCGAACGGTATGCATGGCGGCTACGATTCTC (SEQ ID NO. 184)

.....:Rv192T7.seq:.....  
CGGTGTCGGCACCGGCGTCTTCAGTTGGTAGGCCTGCAGTTTGTGCATCAGGCCGATGCCGCGGCCCTCGTGGCCAC  
GCATGTACAGCACACGCCGCGCCCTCACGGGCGACCATCGCCAGCGCGGCGTCCAGCTGAGGCCCGCAATCGCAGC  
GGCGTGACCCAAACACATCGCCGGTCAAGCACTCCGAATGCACCCGACAGCAGTCGTACCGTCGGCGTTGGGCC  
CGGGCATCTCGCCGCGGACAGCGCGACATGTTCCACGTCTCGTAGATGCTGGTGTAGCCGATGGCGCGAAACTCCC  
CATGACGAGTCGGAATCCGCGCCTCGGCGACCCGCTCAATGTGCTTCTCGTGCTTGCGCCGCCATTTCGATCAAGTCAG  
CAATGGTGATCAGCGCCAGACCGTGCTCATCGGCGAACACCGCAATTCATCGGTGTTGCGCCATCGAGCCCTCATCTT  
TTTGGCTGACGATCTCGCAAATCGCCCCCGCGGGTTGCAGCCGGCAT (SEQ ID NO. 185)

Clone Rv193

.....:Rv193SP6.seq:.....  
ATACTCAAGCTTTGGGTGAAAGCCGATCACCGGAAGCCGCATGATCAGCCACGTTTCGCGCCGCCCGGCATACGGCGG  
CGTACCGATCTCCGCGTCATACACCCGCGGGTAATCGCCGACGGTGCCGGTTCGCGAGCCGAAGGTGACGACGCTGAT  
TGAATCGAGTTCAGGTCCAGCGGGTGGCGCAGCAACGGCGCGAGCTCAACGACGTCAATCACGTTGTCGCTTTCTAC  
GGTCACCGACCCGGTGACCGTNTCGCCCGGTGCGCTCGGCCGATAAGTTGCACCGCCACCACCGCGACACCGTCTTG  
CACGCGGACCCACCCCGGATCCGTTGTTGGCC (SEQ ID NO. 186)

.....:Rv193T7.seq:.....  
AGCTTGCTGGCATCCGCTCCAGTAGCGCCCGCGCGTGGCTTCCAGCGCCCGCAGATGCTCCATGAGCCGGCCGGTTCG  
AGTGGCGCGCGCGGTTACCGCCACCCGCCAGGAGCTGGCGGCCAGCATCTCCGCCCTCACGCATTGCGCGATCACAG  
AGAGAATATACGTCTCATATTGTTGGAGTTCGTGCGAGGCAATCGGTGATGACGGATTTGATGGCATCGAGCTGTG  
CTTCGGCGTAGCCCTCCAGCACGTGCGTATCGTGTGGCGGTCCACGACGACCGCACCGGCGCGCGGACAGCGGTGCG  
GGTTGGACGNTGTGCGGCGATCAGTCCGGCCAGCTCCGCTCGGGATCAGCGGC (SEQ ID NO. 187)

Clone Rv194

.....:Rv194SP6.seq:.....  
ATACTCAAGCTTGCTGCAGCTTCCTATGACTGCTCCCGAAACCTGGGGGTGTGCCTGCTGTGTATGCACGGCATACGG  
ACATCCTTCCCTGAGACCCGCGGTGCAACCCAGCCACGTGTCCATCATCAGGGGTCAACCCCGGCCAAGGGCGACGGC  
ACGCCAAGTTCGCCGACCGTTAACCTAGTGCTGTTAGCTTCATTTGCTGCGAGCAAAACAGCTGGTGGCGCGTTAGGA  
ACTGAATTGAACTCAACCGATTGTTGGTCCGCGCTAGGTGTCTTGGTGGCGGTGCGGCTGGTGTGTCGCGGTGTGGT  
AACNACNACATGTGACCGGGGGAGGTGCAACCACTGGCCAGGCGTCGGCGAAGGTGATTGCGGGGGGAAGAAGAAC  
TCAAAGCCAGTGGGTGACGCGCAGGCCAACGC (SEQ ID NO. 188)

.....:Rv194T7.seq:.....  
AGCTTGACGCGGAGACGACATTGCGAACATTGATGACAAAATAGAAATCATTGATGGTTTGAAGTACCAGGCCGA  
TCAAGCCTTCGCGGAGCCAAATCCAATCAAGAGGCCCAAGCCCGTACCAATCAGCCCGGCAACGAGGGATTCCGTCA  
TTATCAGCCAAAATAACTGCTCTCGGGTTACACCCAAACAGCGCAATATGGCGAAAAACGGTGGCGGTTGCACGACAT  
TAAATGTACGGTATTGTAGATTAAAAAGATACCCACCAACAAGGCAATCAAATGAGAGCGGTTAAATTGACCGTAA



AAGCGTCCGTCATCTGTTTGACGGTGTCCCGTTGGGTATCCGACGTTTCCATACGCACACCGGCCGCGCAGTCTTTGTT  
GGATGCGTGTTGCAGTGGCCTCATCTTTGATGATCAAATCGATGTGGCTCAGTCTTCCGGGCA (SEQ ID NO. 189)

## Clone Rv195

.....Rv195SP6.seq.....  
ATACTCAAGCTTCGGCTCAGGCGGCGCTGCTGGTAAAGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTT  
GGCGGCTACGTGCCATCGAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTACGAGCAAATCGCGGTATGCGTTC  
TTGAGCATGAGTCGGCGACCGTCGTTCATGGTCGACACCCAGACGGAAAGACGCAGATCGCCGTCAAGCATGTGTGCC  
GCGGATTATCAGGACTGACCTCCTGGCTGACCGGCATGTTTGGTCGCGATGCCTGGCGCCCGCCGGCGTGGTGGTGG  
TCCGCTCGGATAGCGAGGTCAGCGAATTNCNTGGCAGCTCCAAAGGCTCCTGCCGGTGCCGGTCTTTGCGCAAACNA  
AGGCNCAGGTTA (SEQ ID NO. 190)

.....Rv195T7.seq.....  
TGATCGCGCATCACCTGCTTCATAAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCAACATGAGCCAGCCTCTCG  
TCGGCGGTTCGGGTGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAACCACTTCATATCCCGCG  
ACGAACGACGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTTCTCCACCGACCGGGCCG  
GGTGTGGGGTGTTCGGCGACCGGCAGCCAGTGGTCCACACTGCCGACGGGCGCCGCGAGCCGTTACCGACCGAGGC  
CGCCGAGCAAGTCCGCCGATCGCATACTCCAACCGGTTGCGGTAAGTGCAGGTTTCAGTGGCGTACTCCTCGTCGCGC  
TCGGCGAGGTCTTGTCCAGCACGTTCGANACGGCAG (SEQ ID NO. 191)

## Clone Rv196

.....Rv196SP6.seq.....  
CAAAGCGGAAGTCTCGCGGACGCCACGACGTGCTGCGTTCGGATTGCCGGCGGCGAAATCAATTCCAGGCAGCTCC  
CGGACAATGCGGCTCTGCTGGCCCGCAACGAAGGACTCGAGGTCAACCCGCTGCCGGGTTCGGGTGCACCTGCCGA  
TCGCACAGGTTGGCCCAACAACCGCCGCTTGATGCCCGGTTCGGCAAGCCCGGCAGTTGCCAAACCCAGCGTGATCAGG  
CTCGGCTCGCGAGTTCCGGGAAGAAGTGGCTCCGCTGATCACCTACCATCCGCCAGGATCTGCGTGTCTTACCACG  
CCGCCAAGGAGGTTGTTGTGGTGCTATCGACCGN (SEQ ID NO. 192)

.....Rv196T7.seq.....  
CCGGAAGCCGCATGATCAGCCAAGTTTCGCGCCGCCCCGGCATAACGGCGGCTACCGATCTCCGCGTCATACACCCGCG  
GGTAATCGCCGACGGTGCCGGTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAGTTCCAGGTCCAGCGGGTGGC  
GCAGCAACGGCGCGAGCTCAACGACGTCAATCAGGTTGTGCTTTCTACGGTCACCGACCCGGTGACCGTNGTCGCCC  
GGTGGCTTCGGCCGAAANTTGCACCGCCACCCGCGAAACCGTCTTGACNCCGGAAGCCACCCCGATCCGTTGT  
TGGGCCAGGTTATTGGGT (SEQ ID NO. 193)

## Clone Rv19

.....Rv19SP6.seq.....  
CCGGAACCGCCGACGGCACGGTATAACGCCTCCGCATATGGGTTCGACAACCAAGCGGGTTCGGACTTCTGGGCTTCTAGC  
GTTTCGCGNGTCGCGACAAACAGCGCGTTCGAACCGACACTCGTTGTGATGTCCTAGCTATCACGTTCCGGTACGCACC  
CAATCGAGTCTAGCGCGGGTAGNTCAGCCCCGATCTCCANGCTCCGCCGAGCCAGGCGC (SEQ ID NO. 194)

.....Rv19T7.seq.....  
CTGGTTTATGTCCCGTTGAAGTTCATCACCCGATGTGGCGGGAGCACTGCCAGGTTCGATCTCAACTACCACATCCGG  
CCGTGGCGGTTGCGCGCCCCGGGGGTTCGGCGCGAACTCGACGAGGCGGTTCGGAGAAATCGCCAGCACCCCGCTGAAC  
CGCGACCACCCGCTGTGGGAGATGTAATTCGTTGAGGGGCTTGCCAACCAACCGGATCGCGGTGGTTGCC  
(SEQ ID NO. 195)

## Clone Rv1

.....Rv1SP6D2.seq.....  
CCGAGCAGTTGGGAATCGCTCTGCANCAAACCAATATTCTGCGCGACGTCGCGCGACGAGCTGGACCGATTAGGCGTA  
GCCTCCGNCTGGACGACACCGGGCACTCGATGACCCCGACGCTACGCTCGCAGGATATTGTTCCCGGACCCCTC  
TCTAG (SEQ ID NO. 196)

.....Rv1T7.seq.....  
TATATAACTCAAGCTTGCCGACGCCAACGCTCGCGCGATGTTGTTAGCCCGACCCGGCTCTTACATGGCACCGGTG  
CCCCACAGCTCAGCCTGTGACGTCCTGCACCGCACTTTTACATAGAATGTGGATTGCGCGATTGGGGATGTCCGGC  
ATCGCTCAATCTGTAGTCCGCTTGTCCCGGAGGGCCATGTGGATGGGGGAAGGATCCGTGGCGTCCGGGATCACC  
ATGGGG (SEQ ID NO. 197)

## Clone Rv201

:Rv201SP6.seq::

ATACTCAAGCTTGCCGAAGTTCCGATGGGTCGCGCCGGCGAGCCCAACGAAATCGCTAGCGTGGCCGTGTTCTTGGCT  
TCGGATCTATCCTCGTACATGACCGGCACCGTGTGGACGTGACTGGCGGCCGTTTCATATGACACCGAGATCATTTGC  
CACGGTACGGAAATTCGTCCAGAAGGAAATCTTCCCAATGCACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGA  
AATCGTCAATCGGCTGGGTGTTATTGGCTTGCTCGGTCGCCGGCTGCGAGGGTTTCTACACCACCGAGTTCATTCTCG  
GGCGTGCCGGCGCATTCGAACCTGGCGGTGCGCGCTG (SEQ ID NO. 198)

:Rv201T7.seq::

GCACCGGCGTCTGCGAGTTGGTAGGCCCTGCAGTTTGTGCATCAGGCCGATGCCGCGGCCCTCGTGGCCACGCATGTAC  
AGCACCCAGCCGCGCCCTCACGGGCGACCATCGCCAGCGCGGCTCCAGCTGAGGCCCGCAATCGCAGCGGCGTGAC  
CCAAACACATCGCCGGTCAAGCACTCCGAATGCACCGGACCAGCACGTCTTCACCGTGGCGGTTGGGCCCGGCGATC  
TCGCCGCGGACCAACGCGACATGTTCCAGTCTCGTAGATGCTGGTGTAGCCGATGGCGCGAAACTCCCCANGACAA  
GTCGGAATCCGCGCCTCGGCGAACCCTCAATGTGCCTCTCGTGCTTGCGCCGCCATTG (SEQ ID NO. 199)

## Clone Rv204

:Rv204SP6.seq::

TGGTCCGTGTGCGCATACCAATAACGCGCCGGGCACCTGACGCGCGGGCCGCAACCAATCGGTGGCCATCGCCATC  
TTCTGCTACCCGGTCAACGGACGCACCTTCTCCTGGCCGACGTAGTGCGCCCAACCGCCGCGGTTGCGTCCCATCGAT  
CCGGTCAAC (SEQ ID NO. 200)

## Clone Rv205

:Rv205SP6.seq::

GGCGTGTGGCCACCGGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCC  
GACTTTCCGCGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAACCTAC  
TTCATCCTGACGCCGGAACAAATTGACGCGAGCGGTTCCGCTGACCAATACGGTGGTCCCACGATGACCCAGTACTAC  
ATCATTGCGACGGAGAACCTGCCGCTGCTAAAGCCACTGGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCT  
GGTTCAACCAAACTTGAAGTGATTGTTTACCTGGGCTACGGCGACCCGGCCTATGGTTATTGACCTCCCCGCCCAA  
(SEQ ID NO. 201)

:Rv205T7.seq::

CGTCCGTGNNCCCTCAANCGCGTGNNGCCGAAGCGGCTGGTTACGACTCCCTGTTTGTGATGGACACTTCTACCAACT  
GCCCCATGTTGGGGACGCCCGACAGCCGATGCTGGAGGCCCTACACGGCCCTTGGTGGCTGGCCACGGCGACCGANCG  
GCTGCAACTGGGCGCGTTGGTGACCGGCAATACCTACCGAGCCCGACCCCTGCTGGCAAAGATCATCACCACGCTCGA  
CGTGGTTAGCGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGTTGGTTTGGAGCTGGAAACACCGCCAGCTCGGCTTCG  
AGTTCCGGCACTTTTCAGTGACCGGTTCAACCGGCTCGAAGAGCGCTACAGATCCTCCAGCCAATGGTCAAGGGTGAGC  
GCCCCACGTTTTTTCGGCGATTGGTACACCACCGAATC (SEQ ID NO. 202)

## Clone Rv207

:Rv207SP6.seq::

CCGCTTCCGTGTAACCGAGCANNGCGAGCGANCTGGCGAGGAAGCAAAGAAGAACTGTTCTGTCAGATAGCTCTTACG  
CTCAGCGCAAGAAGAAATATCCACCGTGGGAAAACTCCAGGTAGAGGTACACACGCGGATAGCCAATTCAGAGTAAT  
AAACTGTGATAATCAACCTCATCAATGATGACGAACTATCCCCGATATCAGGTACATGACGAAGGGAAAGAGAAG  
GAAATCAACTGTGACAAACTGCCCTCAAATTTGGCTTCCTTAAAAATTACAGTTCAAAAAGTATGAGAAAATCCATGC  
AGGCTGAAGGAAACAGCAAACTGTGACAAATTACCCTCAGTAGGTGAGAACAAATGTGACGAACNCCCTCAAATCT  
GTGACAGATAACCCCTCAGACTATCCTGTGTCATGGAAGTGATATCGCGGAAGGAAAATACGATNTGAGTCGTCTGGC  
GGCCTTTCTTTTCTCAATGTATGAGAGCG (SEQ ID NO. 203)

## Clone Rv209

:Rv209SP6.seq::

TGACACCCAACAGAGGGCACTTAAGATGGCAATGCGGCGCCTACCTGCACGTTTTTCGCGATGTCAGAGGATGCCGAG  
GGAGAACAATGCGAGCACGGCCGCTGACNTTGCTCACCGCTTTGGCGGCGGTGACATTGGTGGTGGTTGCGGGCTGCN  
AGGCCCGANTCNAGGCCGAAGCATATAGCGCGGCCGACCGCATTTCTGCTCGACCGCAAGCGGACCTCAGCCGCGAGC  
CGGTGGAGCTACTGTGCGCGCCATCACGCC (SEQ ID NO. 204)

:Rv209T7.seq::

ACGGGCGACGCTGAGGTGGGCCCGGGCTATTGCTGTGCTCCACGTCCAGCGACGCACTGCGCCAGACGGCCCGC  
CAACTAGCCACCTGGGTGGAAGAACACCAGGACTGCGTGGCGGCCTCGGATCTGGCCTACACGCTGGCGCGTGGCCGC  
GCGCACCGGCCGTGCGCACCGCGGTGGTTGCCGCCAACCTGCCGGAGCTCGTCGAGGGTTTGC GCGAGGTGGCCGAC

GGTGACCCCTCTATGACGCGGCGGTGGGACACTGTGATCTAAGACCGGTCTGGGTCTTCTCCGGGCAAGGGTCTCAGT  
GGGCGGCGATGGGCACCCAATTGCTCGCCAGCGAACCAGTGTTCGCGGCCACCATCG (SEQ ID NO. 205)

## Clone Rv20

.....Rv20SP6.seq:.....  
ATACTCAAGCTTCGCGAGATCCGGATGGCACTCACGCTGGACAAGACCTTCACAAAATCTGAAATCCTGACCCGATAC  
TTGAACCTGGTCTCGTTTCGGCAATAACTCGTTTCGGCGTGCAGGACGCGGCGCAACGTAATTCGGCATCAACGCGTCC  
GACCTGAATTGGCAGCAAGCGGCGCTGCTGGCCGGCATGGTGCAATCGACCAGCACGCTCAACCCGTACACCAACCCC  
GACGGCGCGCTGGCCCGGCGGAACGTGGTCTCGACACCATGATCNAAAATTCCTCCGGGGAGGCGGAGGCGTTGCGTG  
CCGCCAGGGCGAACCCTGGGGTTCTGCCGACGCCAATGATTGCCGCGGCTGCATCGCGGGCGGCGACCGCCA  
TTCTTCTGCGAATACGTCCAGGAGTACTGTCTCGGGG (SEQ ID NO. 206)

.....Rv20T7.seq:.....  
AGCTTATGTGGCCGCCACCTACCTTATCTAGCCTAGCTAACTAAATCCAGTGCCGACAGTGCGCGGCTGGCCACCCA  
GCATGAGGTTATGACCACGGCATATGCCAGCGCGCTGGCGGCGATGCCGACGCTGACCGAGTTGGCCGCTAATCACAC  
CAGCCATGCGGTGTTGCTGGGAACGAATTTCTTTGGAATCAATACGATCCCGATCGCGCTCAATGAGGCCGACTATGC  
GCGGATGTGATTTCAGGCGGCCACACGATGAGTATCTATGAGGGCACCTCCGATGCGGCGCTGGCGTNGCACCAGCA  
AACCACACCGGCTCCGGTACTGTTCAACGGCGGTGCTGGCGTTTGCCAGCGCTGCCGCGGATCTC (SEQ ID NO. 207)

## Clone Rv214

.....Rv214SP6.seq:.....  
ATACTCAAGCTTGCCACCCATGCCGAGCAAGGTCGACTCAGCGATGACGAATTGTTCTTCTTCGCGGTGTTGCTGCTG  
GTTGCGGGCTATGAGAGCACTGCTCATATGATTAGCACNTTGTTCGACGCTGGCCGACTATCCAGATCAGCTGACA  
CTCCTTGCGCAGCAACCAGACCTGATCCCGTCGGCGATCGAGGAGCACCTCCGCTTTATATCGCAATCCAAAACATCT  
GCCGACAACGCGCTGACTATTGCGTTCGCTCAAGCGGTCAATCCCGGA (SEQ ID NO. 208)

.....Rv214T7.seq:.....  
CCGGGGTAGAACGATGCGATCTGGGCCATGTCGACATCGGTGGTACAGGTAAACCGCGCCGTGTGCGCGGTCTCGGAG  
ATCAGAACGTGGTCGAGTTGACACCGCGGGCTTTCAGCCAGTCGCGATAATCGGCGAAGTCGGCGCCTGCCGCCCA  
ACTAGCGCGACCTCGCCACCTAGCACACCGATGGCGAAGGCCATGTTTCGGCCACGCGCCCGGTCATCATCAAC  
TC (SEQ ID NO. 209)

## Clone Rv215

.....Rv215SP6.seq:.....  
ATACTCAAGCTTGGCGGCAACGCCACTACCGGGCTCACCAGGTCTGTGCCGCCACCGCCGGCGCCGAAAGCACCATC  
AGGTCGTAGTTGTCTGGACGTTTCGACACCGTAAGCGAACAACAATGCCGCCGCCATGCTGTGCCCGAGCAGATGCGC  
TTGTCACCCGGGATATTCGCGGTGGCGATCCCAACGAGGGTGTGGAAGTCAGCGGTGTATCTGAGATGTCTCTACTA  
TCATCCGTTTGGCACCCGAGCGGGCATGCCCGCGGGGGGTCAAC (SEQ ID NO. 210)

.....Rv215T7.seq:.....  
GTGACGGCATCAAGGTCCGAGTGATGGTGTTCATCTACCCAGGAAGGCGTGAAGTGGCTGATACCGTGGCTTGAG  
GATTCGGTGC GGTCGCCAGTTAATCCGCCGTGTGCTCCGGATGAGCGCGACGGTAACCTGGAATTGTGCTGTGTGC  
TGGCTGTGTGTTGTGATGAGCCTGTCTAAGTGGTGCCTAACCGTTTTCAGGACCGCGGCGCTCGCTGCAAACATTGAA  
GCCCCACGCTCTGGGTTTGTATTTACACAACGAGGGCGCTCCCCGATCTGGCGCGCGCAACGAGGTGCNCACTATCCA  
TTCGAGGTGAACTGGACTCCTTGATGCTCATGCCGGTTCGGTTCGCTGTC (SEQ ID NO. 211)

## Clone Rv217

.....Rv217SP6.seq:.....  
ATACTCAAGCTTGCCTTCGATGAAGTAGTCGTCGGTCAGCGCCGCTCTTCGAGCTCCTTGGCGATGCCAGCAAGGA  
GTATCGCCCGGAGCTTGGCCAGGATCTTGTCCGCTGTTCTTTCGAGATGCGGGCCCGCGGATCGTAGTTCTTGTGA  
GACACGATGACCGAAACCCATCAATTTGACCCCGGCTCGCGGTTCTTGACCTTGCGTTACAACTCGTGACGTCGT  
CGCCGCTGTGCGAATGCCCTC (SEQ ID NO. 212)

.....Rv217T7.seq:.....  
NGTCAAGCCGAGCATGCGCGAGGNAACGACGAACCAAGCCATGGTGGTTGGCGCCGTCGAGAGGTGGCGGTGCG  
CCACAACGGGAAGATCGCCTTGAGCGTCGCTCGACCGCGCCTCGAGTTGGGTGATAACGAAGTAGTGTGATGCEGATC  
ATGTCGACGTTTCCGTCGATCAGCGTGCAGCGGCGACCACTCGACGAGGTCTCGGTGCCGCCCGCGGCCAGGGCACC  
AGCAGTGACGATTCCAGGCGCCGTGCGG (SEQ ID NO. 213)

## Clone Rv218

.....Rv218SP6.seq:.....  
CGATAATCGCTTCCGGTAAGTGCAGCAGCTTTACGACGGCGACTCCCATCGGCAATTTCTATGACACCAGATACTCTT  
CGACCGAAGCGCGGTGTCTGTTGACCACTCAGTAGAAAAGAAGGGATGAGATCTCCCCGTGCGTCTCTAGTAAGCAGC  
TCCTGGTCGCGTTCATTACCTGACCATACCCGAGAGGTCTTCTCAACACTATACCCCGGAGCACTTCTAGAGTAAAC  
TTCCCATCCCCGACCATATAGGCTAAGGTAATGGGCATTACCGCGAGCCATTACTCTACGCGCGCAATTAACGAAT  
CCACCATCGGGGCCGCTGGTGTCTN (SEQ ID NO. 214)

## Clone Rv219

.....Rv219SP6.seq:.....  
NAATACTCAAGCTTTCTCGTGATTACCAACCCGTGTAATTTGGGATGGGCAAAAAGGCGAATCACCGCGTGGCCACAAA  
CGCCGGGAGGGACAATCTCGGGCGGCTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGCTC  
GCCCTCCGACCGCAACATTCGGGGATGGCAGCAACCTGGTATCACCTGGCCGGGCAATGATCTGACGCGTGGCCGC  
GGGTAGTGNCCGCCCGGGCGGCTAC (SEQ ID NO. 215)

.....Rv219T7.seq:.....  
CCAACCTAGAGCATCGGGACATACGGAGTCAACTACCCGCCAACCGGTGATTTCTTGGCCGCCGCTGACGGCGCGAACG  
ACGCCAGCGACCACTTACGAGATGGCCAGCGCGTGGCCGGCCACGATGTTGGTGTCTGGCGGCTACTCCCAGGGTG  
CGGCCGTGATCGACATCGTCACCGCCGACCACTGCCCGGTCTCGGGTTCACGCAGCCGTTGCCGCCCGCAGCGGACG  
ATCACATCGCCGCGATCGCCCTGTTGGGAATCCCTCGGGGCCGCGCTGGCGGGGTGATGATCGCCCTGACCCCTCAA  
TTCGGGTCCAAGA (SEQ ID NO. 216)

## Clone Rv21

.....Rv21SP6.seq:.....  
ATACTCAAGCTTGCTGCAGCTTCTGTGACTGCTCCCGAAACCTGGGGGTGTGCCTGCTGTGTATGCACGGCATAACGG  
ACATCTTCCCCTGAGACCCGCGGTGCAACCAAGCCACGTGTCCATCATCAGGGGTCAACCCCGGCCAAGGGCGACGGC  
ACGCCAAGTTCGCCGACCGTTAACCTAGTGCTGTTAGCTTCATTTGCTGCGAGCAAAACAGCTGGTGGCCCGTTAGGA  
ACTGAATTGAAACTCAACCGATTTGGTGGCGCCCGTAAGTGTCTGGCTGCCGCTGCGCTGGTGT  
(SEQ ID NO. 217)

.....Rv21T7.seq:.....  
AGCTTGCGCGCGCTGGCGATCGCGGTTCAAGGCGCGCTCTTCGAGCACAACGAGCGAAGACAGCTCGGCGACGGAGCC  
TTTATCGACATCCGTTCCGGCTGGCTGACCGGCGGCAAGAAGTGTGGACGCGTGTGTGTCGACGGTGCCGTGGCGA  
GCCGAGCGCGCTCAGATGTACGACCGGGTGGTGCATGTGCCGCGGCTGGTGAGTTTTCACGACCTGACCATCGAAGAT  
CCGCCGCATCCGACGCTGGCGCGGATGCGCC (SEQ ID NO. 218)

## Clone Rv220

.....Rv220SP6.seq:.....  
AATACTCAAGCTTGCGCACGACCAGGACGTGAGTGGCGCTTGCACTGACTTGGCGACCTCAAAGGCCACCGGTACCC  
CGCCGCGCGGCAAGCCAAGGACNACNACGGCCTTGCCGGATAGCTGCGCCAGGCGTTGCGCCAACCTGGCGTCCAGCGT  
CGCCACGATCGTCAAAGAGCTTCATCTGCCGAGTGTGTGCCATCTCATGGCTCCAAATATGGAATTAGGTCCCTGGG  
CCGACTGACGACAGTCCCTCAGCGACCGGATTGCGCATCCCGCCTTGACGCTGCTCCGCAAATCCCGGGCTTGGCTC  
CGCGGAAGCGAACTCGGCGGCGCTACGGTGGTGGCTCACTTCGGCCGTGC (SEQ ID NO. 219)

.....Rv220T7.seq:.....  
GGTTGGTGGGTCCACCTTCGCGGCGGCGCGATATGCCTTGCTGGTCTTGTCTCATTTGATATCCAATCTATGGGT  
CGTGGTTACTCAGCGGGCCGAAGCTGGCCCTCCACGGGTAGGGCCCTATTGACGGGTGATGCCATCGACCGAGCGG  
TACCGGCGATGATCTTGGCCGACGCTGACGTCGTTGGCGTTGAGGTCCGTCTTCTGGTCTCGGCGATTTGCGGGA  
CTTGATCCCAGGTGACTTTGGCGACCTTGGTCTTGTGCGGCTCCGCCGAACCTTCGCCACACCAGCGGCCTTAAGCA  
GCAGCTTGGCGGCGGGCGGCTCTTCAGCGTGAAAGTGAAGCTACGGTCTTCATAAACGGTGATCTCCACCGGGATGA  
CGTTGCCGCGCTGGTTCTCCGTGCGGCGGCTGTACGCCTTGCAAGACTCCATGATGTTGACCCGTGCTGACCGAACGC  
GGGCCCCACTGGCGGGG (SEQ ID NO. 220)

## Clone Rv221

.....Rv221SP6.seq:.....  
ATACTCAAGCTTTTCGACCCGCAAGCCGGCGGTGCCCTCCTCGTTCCGCTGCCCGGTCTGCTCGATCGGTTCCGGGT  
CGCCGCGCTAGGCCCAATTGCCCGGCTCCTCCTCGGGCGGTTCCACAACCCGCATCGTCGCCGGGCTAGGTTCAAGCC  
ATGCCGGTAACCCAGGACGCCAGTGCTGATCGGCTATGGACAGGTCAACCACCGAGGCGACATCGACGCCNAAAT

CAGTCCATCGAACCCGTCGACCTGATGGCCNCCGCGGCCCGGAAAGCCGCCGAGTCCACCGTGCTCGAAGCGGTGGAT  
TCCATCCGTGTGGTGCACATGCTGTGCGCGCATACCAGGAATTCGCGGGCGTCTCCTCGGC (SEQ ID NO. 221)

.....Rv221T7.seq:.....  
NCCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCGGCGGTTCGGG  
TGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAACCAGCTTCCATATCCCGCGACGAACGACGCC  
AGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTTCTCCACCGACCGGGGCGGGTGTGGGGTG  
TTCGGCAACGGCAACCAAGTTGGTCCACACTGCCGACGGGCGCCGCAATCCGTTACCGAACCAGGCCGCCNAAACA  
ATTCGCCCCGATCCCATAT (SEQ ID NO. 222)

Clone Rv222

.....Rv222SP6.seq:.....  
ATACTCAAGCTTGTTCGGGATCAATCTCGAGGGCATCCACGCACGAAAAGTAAACTCTATCAAGCTTTTTGACGACACC  
CACGGACGCCCCATATATGTTTCGGGTGGGCAAGACGGTCCCTACCTGGAACGTTTGGTGGCCGGCGACACCGGTGAG  
CCCACGCCGCGACGGGCCAACCTCAGCGACTCGATTACCCCGGACGAAGTACTCTACAGGTGGCCGAAGAGCTCTTT  
GCCACACCGCAACAGGGACGGACTTTGGGCTTGACCCAGAAACCGGCCACGAAATCTTTCAGGGGAAGGCCGTT  
TGGGCTTATGTTACCTATATCCTGCCGGAACCTGCGGCTGATGCGGCCGCGCCGCTCAGGGAN (SEQ ID NO. 223)

.....Rv222T7.seq:.....  
AGCAGCTAGCCGCGCTCGCCGCGCTGGTTCGGTGCATGCTCGCAGCCGGATGCACCAACGTGGTTCGACGGGACCG  
CCGTGGCTGCCGACAAATCCGGACCACTGCATCAGGATCCGATACCGGTTTCAGCGCTTGAAGGGCTGCTTCTCGACT  
TGAGCCAGATCAATGCCGCGCTGGGTGCGACATCGATGAAGGTGTGGTTCACGCCAAGGCAATGTGGGACTGGAGCA  
AGAGCGTGGCCGACAAGAATTGCCTGGGCTATCGACGGTCCAGCACAGGAAAAGGTCTATGCCGGCACCGGTTGGACC  
GCTATGCGCGGCCAACGGCTGGATGACAGCATCGATGACTCCAAGAAACGCGACCACTACGCCATTCAAGCGGTCGTC  
GGCTTCCCGACCGCACATGATGCCGAAGAATTCTACAGCTCCTCCG (SEQ ID NO. 224)

Clone Rv223

.....Rv223IS1081N1400.seq:.....  
CGCGACTGGCTCCCCGGNCGGCTGCTCGGGTCCGCCGATAGAGACCGGGATGTCGCCCCGACGACGGGCAGCCGGGTTG  
CGTGGGACGGGGCGGGGTTCGGGCAGCCCAAGCAACGGGCTAGTCCCCGAATCCTACGGAGCCGTACCTACGCCTAC  
GTAATAGTAGCTATCAATAACAGTTGACATACGCAACGATCTGTGAGATCAATATTGCCTGACGCATGTCAAGACAGG  
CGTCAAGACAGGTGTCAATAATTGCTCCGCTGGTGACGGTAACCGGTTCGTGCGGGTGTGTGACGCCTAAGGAAGGAG  
TGTGGGTGGTGACGCTGAGAGTGGTTCCTGAGGGTTTGGCGGCCGCCAGTGCGGCGGTGGAGGCGTTGACCGCACGGC  
TGGCCGCCGCGACACGCTGGCGCGGCGCCGGCGATTACGGCGGTGGTGGCGCCCGCGGGGATCCGGTGTGCTTGCAGA  
ATGCGGTGGGGTTTAGCGCCTTAAGTAGCCAGCATGCCGCGATCGCCGGCGAAAGGGTCCAAGAAGTGGGT  
(SEQ ID NO. 225)

.....Rv223SP6.seq:.....  
ATACTCAAGCTTATTGAACCGCGGGTCGCGAGGCAAGTGACCTCATAACGACTCGGGTCCAGCGACCGCGCCAAAC  
GAACGGCCGGACGACGTGGGCCAGGGTCGCGGCCCTCCCTACAAACAGGATCCGTTGCCTGCGAAGCAGAGGCTCCGG  
TGCGGCGTTGGGCGCCGTGCTGCTCCAGCGTCCGGTCCCGGGTCGCCGGCGACGCTTGTTTCTCCATACTCGCCCC  
CTAATCTCGAGGCGAGCCCGTACCCGCGAGGCAACCTCCCAAAATGCAATCCCGCAAAATGCAATGCGTCNAGCTATTT  
CTCACACCGACCGTAGTTGCGGATCAGAAATCCGTTGGGCGCGGAAGTCCAGCGGAATTTGTTCTCCCGCTCCGCAT  
CATGCTTGTAATCGTTTGGAAATTCATCCTCATATGCCTCGATCGCTTCATAGGGTCCAGGCCAAACCCGGCGAGGA  
CTGGGTGGCGGTTGATGTTGGAATCCTCCACTACTAGGTATTCACCGGC (SEQ ID NO. 226)

.....Rv223T7.seq:.....  
GTCTCGATCATGGCCAAAGAGCTCGACGAAGCCGTAGAGGCGTTTCGGACCCGCCGCTCGATGCCGGCCCGTATACC  
TTCCTCGCGCCGACGCCCTGGTGCTCAAGGTGCGCGAGGCGAGCCGCGTTCGTGCGGGTGCACACCTTGATCGCCACC  
GGCGTCAACGCCGAGGGTACCGAGAGATCCTGGGCATCCAGGTCACTCCGCCGAGGACGGGGCGGGTGGCTGGCG  
TTCTTCCGCGACCTGGTCGCCCGCGGCTGTCCGGGGTGCAGCTGGTCAACCGGCGACGCCACGCGGCGCTGGTGGCC  
GCGATCGGCGCCACCTGCCCGCAGCGGCTGGCAGCGCTGCAGAACCCACTACGCAGCCAATCTGATGGCAGCCACC  
CCGAAGCCCTCCTGGCCGTGGTGCGCACCCGTGGTGCATCTACGACCAGCCGACGCCGAATCAGTTGTTGCC  
AATATGATCGGGTCTCGAC (SEQ ID NO. 227)

Clone Rv224

.....Rv224SP6.seq:.....  
ATACTCAAGCTTTCGTGAGTTCATGGCGCCAGCAGACCAACAGAGCATCGGGACATACGGAGTCAACTACCCGGCCA  
ACGGTGATTTCTTGGCCGCGGCTGACGGGCGCAACGACGCCAGCGACCAATTAGCAAATGGCCAGCGGTGCCGGG

CCACGAGGTTGGTGCTCGGCGGCTACTCCCAGGGTGCGGCCGTGATCAAGATCTTCACCGCCGCACCACTGCCCGGCC  
TCGGGTTACGCATCCGTTTGGCCGCCGCC (SEQ ID NO. 228)

.....Rv224T7.seq:.....  
GCCCCGTGTAATTTGGGATGGGCAAAAAGCGAAGCACCGCGTGCCACGAACGCCGGGAGGGACAATCTCGGGCGGCT  
AGGGCTTCTCGCGGGAAGGCCGAACGTACGGCGTTTCAACACGTGCGCTCGCCCTCCGACCGGAACATTCGGGGAT  
GGCAGCAACCTGGTAGCACCTGGCCGGGCGATGATCTGCAGCGTGC CGCGGGTAGTCTCCGCCCGGGCCGC  
(SEQ ID NO. 229)

Clone Rv225

.....Rv225SP6.seq:.....  
ATACTCAAGCTTCTTTGACCGAACGCGTCCACCGCACCGTGAGATTGGTGGCGCCATTTCGTGCTGGTGTAGCTGCTG  
TTGGCGGCGTCGCCGTATTGTGCGGGCCAGCCTTGTGCGGGGGCCGCTTCTACCCACAAGTCGGCACTTCGCAACCG  
CCCAGCTCGACCGGAATTACGGCGGCGCAACGCGCCCGGAAGGCGTCACGCAATCGCTTATCCTTCCAGGTTCC  
CAAATCCTCCGCTTACTTGGGTCCTTCATCGG (SEQ ID NO. 230)

.....Rv225T7.seq:.....  
GGCAGCGGCGACAACCGGAACGTCCGCACGGTGCTCAATCACGGGTGCACGGTGTGCATCAGAATGGCGGGGGTTCGT  
TGTCGCGGTGAGGCGTTTCGGCGAGGAGGTAGTGTCTACCCCTTGC CGCGGGTTCGTGCGGACTGAAAGGGATTTCAT  
TGGGAACCCACGGCTGCGTATCGCAGGGCCTCGGTGACGTCTGCTTCTCNAGCTCAGGAAGTTTCGGCGAGAATCTCG  
GTGGATGTTATTTGGTCCGCTAC (SEQ ID NO. 231)

Clone Rv226

.....Rv226SP6.seq:.....  
ATACTCAAGCTTCTTCGGCTTCTCTGATAGCCTGAGAAGAAACCCCAAGTTAATCCGCTGCTTCACCTATTCTCCAGC  
GCCGGGTATTTTCTCGCTTCGGGCTGTATCATTAATACTGTGCAATGGCGATAGCCTTCGTCAATTCATGACCAG  
CGTTTATGCACTGGTTAAGTGTTCATGAGTTTCATTCTGAACATCCTTTATTTCATTGTTTTGCGTT  
(SEQ ID NO. 232)

Clone Rv227

.....Rv227SP6.seq:.....  
ATACTCAAGCTTGGTGACCGGCACCGGATACGTTGCGGCAGGCATCTGGGCTGGCGGTGGTTCGCCGCTCCGAAGCC  
GTCGAACACCATCGCCAGCGCGGCTTCCACATCAACGACCATTTTCGGCCAGCTTGC GGCGCATCAGCGGCTTGTGAT  
GAGCGCCCCACCGAATGCCCGCCGCTGCCCCGGCGTATCACATCGATTTCGACCATCGCGCGGGCGCGCTTGCCGAGGGC  
GAACGAGGCGGTGCCCAACCGCAATCTGTTTGGTCAGCTCCCTCATGCGGGTGATTCTTGC CGTCCGGACGGGCCC  
CGGTATGCGCTCGGTTCCGC (SEQ ID NO. 233)

.....Rv227T7.seq:.....  
CCGTTGCGCAGCGTGAGCCGATAGTTGACATCCGGCTCGGTGAAGGTGAAATCGATGGCCAGGTCGAGGTCCCATGCG  
CGTGGGCCATTGATGCTGATCGCCAGGACGTCAAAGATTTGGTCCGGCGTCAGCTGGGCGAAAACGTGGGCGCCGGG  
ACTTGCCCGGAGCTGCCCGGGTTCCCGTCCGCGCAGCTCGCGGGCCCCGGTCAGAAAGAAATTGCGCCAGGTCGCACAC  
TCCGCGCCGTAGGCCAGCTGCTCCAGGGTGTGCGCATAGAGCCCCGGGGCCGACGCGTGTCTGCTGTCGGCGAACACC  
GCATGGTCGAGAAGCGTTGCCGCCCAACGGGAAATCACCTGCGTCGAAAGCTTCGCGGGCCAGCTCCAGCACTCGGTC  
GATGCCACCCAACGCGT (SEQ ID NO. 234)

Clone Rv228

.....Rv228SP6.seq:.....  
ATACTCAAGCTTGGCGATGTTACCCCTGACAGCGTGAATGTGTCNAAACACACGGCACCGGAACGGTGTGGGGGAC  
CCCATCGAGTTCGAGTCGTTGGCGGCCACTTATGGCCTGGGTAAAGGCCAGGGCGAGAGCCGTGCGCATTTGGGGTCG  
GTCAAAACCAACATCGGCCACCTGGAGGCGGCGCGGTGTGGCTGGATTTCATCAAGGCGGTGCTGGCGGTGCAACGT  
GGGCACATTCCCCGAACTTGCACTTCACCCGGTGAACCCGGCCATCAACACGTGCGCGACGCGGCTGTTCGTGCCG  
ACCGAAAGCGCCCCGTGGCCGCGGCTGCCGGTCCACGCAGGGTGC GGTTGTCATCGTTCCGGCTCAGCGGGACCAA  
(SEQ ID NO. 235)

.....Rv228T7.seq:.....  
CCGGTAACCAGATCAGCTCGTCGACCTCACTGCCGGGGTGAATTTCCCAACCGGTGCTGCGCGCTGCCAGTAGTGCA  
CCTTCTTGACGCCTCGAAAAGGGGAGTCGGTCCGGTAGGTACCGTCAGGAGCCGCTACCCAGGTTGGCGCGGTGAC  
CGGTCTCCTCGAGTATCTCCGCAACGCCCCCCACCGGTGCGGTCTCGCCCGGATCCACTTTGCCCTTGGGCGAGCGACC  
AGTCGTCGTAACGGGGGCGGTGAATGACAGCGATCTCGACCGGCCCTTCCGAATCGGCACTGCCGGGTGCCAGAAC  
CCGACCGCGGCGGTACACAATCCGGCCGCGGAGCGCGGGCGGACGANTTCTGGATCGACACCTCAACTCCTG  
CAGGTCAATTCGGCCAAGCTGCTCGCGGTGCTGGATGTGGT (SEQ ID NO. 236)

## Clone Rv229

:Rv229SP6.seq:::

ATACTCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCACCCACCACGCGCGGGTCGGGCGCCGGGCCCCGG  
GCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCCGGCTGCGCTACGTCGAGCCATACCGGGCG  
GAGCTACATCGGCTCGGCCGCCAGTGTTCCGGGCCCTCTTTCGAGGTCGAGGCTATACCGATTGCGCATCCGCAGC  
CGCACCTGGTCGTCTCGTACCGTGCCCTACCTCTGCTTGTCCGGCGGGGCCA (SEQ ID NO. 237)

:Rv229T7.seq:::

TCCGTACGGCCCCGGGTACGCTTCGGTCGCAGTGTCGAGTGATAGATGACGACCGGGACCTCGTCGGCATCTTCCATA  
GCCCCCACACCTTCAGTTGCTCACCGGAATCCAACCGGTAGAAGGTCGGCGAGCGCTCGGCATTGGTCATCGGGATA  
TGCCGCTCGGGACGGTCAGAGCCCTCGGGTCGGCCAGCACTCCGCAGGCTTCGTCGGGGTGGTCGCGACGCGCATGG  
GCCACCATCCATCCACCAGGTCTGCGCGAATCACCCGC (SEQ ID NO. 238)

## Clone Rv22

:Rv22SP6.seq:::

GGACACATTGCGAACATTGATGACAAAATAGAAATCATTGATGGTTTGAGTCACCAGGCCGATCAAGCCTTCGCCGAG  
CCAAATTCCAATCAAGAGGCCCAAGCCCGTACCAATCAGCCCCGCAACGAGGGATTCCGTCATTATCAGCCAAAATAA  
CTGCTCTCGGGTTACACCCAAACAGCGCAATATGGCGAAAAACGGTCGCCGTTGCACGACATTAAATGTCACGGTATT  
GTAAATTAAAAAGATACCCACCAACAAGGCAATCAAACCTGAGAGCGGTTAAATTGACCGTAAAAGCGTCCGTCATCTG  
TTTGACGGTGTCCCGTTGGGTNTCCGACGTTTCCATACGCACACCGGCCGGCAGTCTTTGTTGGATGCGTGTTCAGT  
GGCCTCATCTTTGATGATCA (SEQ ID NO. 239)

:Rv22T7.seq:::

GCCTGGCCAGGTGAAGGCCGACCTCGACGCCAAAGCCGCTGATCCGGCACATGAGTCGGTGGACTGGGACTTGAAGT  
CGCTGCGATGGGCGTGGAACCGAGCCAAAGATGACGTGGCGCCGTGGTGGGCGGAGAATTCCAAGGAGTGCTACTCGT  
CGGGGTTGGCCGATCTGGCCAGGGCCTGGCTAATTGGAAAGCTGGCAAGAACGGGACCCGCAAGGCCGGCGGGTGG  
GCTTCCCGCGATTCAAATCCGGGCGGCGTGATCCTGGCAGGGTGCGGTTCAACACCGGCACCATGCGCATAGAGGATG  
ACCGGCGCACGATCACGGTCCCGGTGATCGGGCCGCTGCGGGCCAAGGAGAACACCCGCCGGGTGCAACGCCACCTCG  
TGAGCGGGCGCGCGCAGATCCTGAACATGACCTTGTGCGAGCGGTGGGG (SEQ ID NO. 240)

## Clone Rv230

:Rv230SP6.seq:::

TAACTCAAGCTTCAAGTCCGNGTCCGACCCTGTTTCGACGGCTACCTGAATCAACCCGATGCCCCGCCGCGGCGTTCCG  
ACCCGACAGCTGGTACCGCACCGGCGACGTGCGGGTGGTCGACGGCAGTGGGATGCACCGCATCGTGGGACGCGAGTC  
GGTCGACTTGATCAAGTCGGGTGGATACCGGGTCGGCGCCGGTGAAATTGAAACGGTGCTGCTCGGGCATCCGGACGT  
GGCGGANGCGGCAGTCGTGGGGTGCTCGACTATTATCTAGGCCAGCGGATCGTTGCCTACGTAGTCGGCTCAGCGAA  
TGTCGATGCGGACGGGCTTATCACTTTGTTGCCCAACAACTTT (SEQ ID NO. 241)

:Rv230T7.seq:::

CCATGTCGCCCAACATATCGTCGATGTTTCGCGTCTCGCCTCGCGCACGTGGTCTGTCACCAGTCAACGTTAACGCC  
GCCGCACATGTCTTCGGCCGGGCAAAAACGTGAAAAACGAGCGGGCGACTGCAATGTCATGACACCGACGCCGCCGA  
TGGGCCAGGGTCTGGCAGATTCGATCTGTGCGGCCAGTGCCAGCAGCGTCGCCTCGTCATACGGCCGGCCGACGAGT  
TGAACCGACATGGGCATGCCGTGCGCGTCAAGTCCCACGGCACACGGCCGCGGGCTGGCCGGTCAGATTCCANACT  
TGAAAGTACTGAAGCCGCTGCACCACAG (SEQ ID NO. 242)

## Clone Rv231

:Rv231SP6.seq:::

CGAAAGCGTGAAACAGCTCGCGGCAGCCCCGACGTGCTGCGTCGGATAGCCGGCGGGCGAAGATCAATTCCAGGCAG  
CTCCCGGACAATGCGGCTCTGCTGGCCCCGAACGAAGGACTCGAGGTCACCCCGGTGCCCGGGTCTGGTGACCTG  
CCGATCGCACAGGTTGGCCACAACCGGCCGCTTGATGCCCGGTGCGCAAGCCCGGCAAGTTCGCAAACCCAGCGTGAT  
CNTGCTCNGCTCTNTANTTCGGCGAAGAAGTGGCTCGCCTGATCACCTACCATCGGCCAGGATCTGCGTGTATCACA  
ACGCTCGCCAAGGAGGTTGTTGTG (SEQ ID NO. 243)

:Rv231T7.seq:::

TCCGCCACGCTTCGCGCCCGCCGGCATACGGCGCGTACCGATCTCCGCGTCATACACCGCGGGTAATCGCCGACGGTG  
CCGGTTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAGTTCCAGGTCCAGCGGGTGGCGCAGCAACGGCGCGAGC  
TCAACGACGTCAATCACGTTGTGCTTTCTACGGTCACCGACCCGGTGACCGTAGTCGCCCGGTGCGCTCGGCCGAGA  
AGCTGCACCGCCACACCGCGACACCGTCTTGACGCGGACCCACCCCGGATCGGTTGTTGGCCAAGGTAATTGGGTC  
ATTCCATTGACGGGACGCCGACCC (SEQ ID NO. 244)

## Clone Rv232

::::::::::Rv232SP6.seq::::::::::  
CATTCTTTAACAGTTGTTTTGGGCTCGGCATGGTTAGCCAACGTTCTGCGGTCCACCATATCATCTTGGTCCGGTAGC  
GCTCGTCCGGGGTATGCTGCCGCCGGGATTCTCGTGCTATTACTCCCCCGAAGAACCGCCACCGGTCCAGCGCGTG  
GGCCGNCGCGGTCCCATCACAACTGAACCCCCAACAGGGACATGCTTATCGGTAGGGCGCGCGCCAAGGCGGCAGCA  
ATCGCATCACTGCGCTCTGCGCGTCACTATTAACCCACCCGGACTTCACTTCCACCACCCCGAATGGCGCCCGGTCTAT  
TGATCATCTGGCGCACCGCGGATAA (SEQ ID NO. 245)

::::::::::Rv232T7.seq::::::::::  
CGGTGTCCTGCAGTTGGTAGGCCTGCAGTTTGTGCATCATGCCGATGCCGCGGCCTCGTGGCCACGCATGTACAGCAC  
CACGCCGCGCCCTCACGGGCGAACATCGCCAGCGCGGCGTCCAGCTGAAGCCCGCAATCGCAGCGGCGTGACCAAAC  
ACATCGCCGGTCAAGCACTCCGAATGCACCGGACCAGCACGTCGTCACCGTCGGCGTTGGGCCCCGGCGATCTCGCCGC  
GGACCATGCGCGACATGTTCCACGTCCTCGTANATGCTGGTGTAGCCGATGGCGCGAAACTCCCCATGACGAGTCGGA  
ATCCGCGCCTCGGCGACCCGCTCAATGTGCT (SEQ ID NO. 246)

## Clone Rv233

::::::::::Rv233SP6.seq::::::::::  
CGGCATCTGGCGGCTGAACCTGTTCTTGGGCAACATGCCGAGGATCGCCTCTTCCACCACGCGGTCCGGGTGGCGTTG  
CATTACCTCACCGATGGTGCCTTGTGCAGGCCGCGGGGATACCCCGAGTGCCGGTAAACCATCTTGTGCTGCAGTTT  
GTCGCCGCTGATGGCGACCTTGTGCGCGTTGATCACGATNACNAATCACCGCCANCGACATTGGGGGCGAACGTCGGC  
TCGTGCTTGCCGCGCAGCAGGCTGGCCGCCGCGACGCAAGGCGCCAACCACACGTCCTGGCGTCGATGACGTACCA  
CCATCGCGTGGTGTACCCGCCCTTGGG (SEQ ID NO. 247)

::::::::::Rv233T7.seq::::::::::  
GCGGCAAAAATTGAAGCACTCNTGGCCACTNCCGCCGGGAGGGACAATCTCGGGCGGCTAGGGCTTCTCGCGGGAAGG  
CCCGAACGTACTGCGTTTCAACACGTCGCGTCGCCCTCCGACCGCGAACATTCTGGGATGGCAGCAACCTGTTAGCAC  
CTGGCCGGGCGATGATCTGCAGCGTCGCCGCGGGTAGTCGCCCCGGGCGGCTACAGTCTGAAACGCGATGACCATC  
GATGTGTGGACGCCGATCCGACNCAACGGTTCCTACACTGTGATATGTTGCGCTCGCTGCGCCGGTGGACGGTGGGT  
CTATCCCGGA (SEQ ID NO. 248)

## Clone Rv234

::::::::::Rv234SP6.seq::::::::::  
CGCGTTGAACTGAAGGGGTGCCGCCGGCTCGAGCAGGCAAGCCATTTGTTTCGATGCGGTTACCGAAGATCTCTTCGG  
TGACTGCCCGCCGCCGGCCAGCTCGGCTCAGTGTCGGCGTTGGTTCGCCGCGGCGACAATCTTGGCGTCCACGGTGGT  
CGGGGTATGCCCGCGAGCAGGATTGGCGAGCGGNCGGTCAGCCGGGTGAATTCGTCAAGAGCTGACGCTGCGGTTG  
GGGAGGCGAATCATGGTCGCTAGCCTCGACTAGGCCCGG (SEQ ID NO. 249)

::::::::::Rv234T7.seq::::::::::  
TGACAACGCGGCGGCGATTACCCCGCTACCGCAGCAGCATGACGCGGTAGCGAACACCGCCGGATGCAGCGCAGGTGC  
GTCGATGTGCTCACGGAATCGCCCCGGCACCGCATCTCGAGGATCACCAGTGCCACCCCTGCAGCGCGACACCGAC  
GATTCGTACACCGCCACGCCGATCAGGCCCTGGGCCAGCTGATTGGAGCTGGCGTATATGGCGCGCATGGTGACGAT  
GGTCATCGCCTCTTACATTGTGGCGGCCAGAACACGGCGTTGGGGCGGCGGTGATGAACACTAGGCGACCANATCC  
CCGGGGTCAACAGTTGACCATCC (SEQ ID NO. 250)

## Clone Rv235

::::::::::Rv235SP6.seq::::::::::  
CGCGGACATCCCGAACGAGGACACGCGACCGCTTCGGTGTGTGATCTATCAGGGCTCGCACCACGCGCAACCGCTTCC  
GGCTACCTAGACGCGGT (SEQ ID NO. 251)

::::::::::Rv235T7.seq::::::::::  
GCATGCGGGTGATGCCGTTCTCAGTGCGCAACAGCGTTCGACGCGGCATACCCAGCCGCACATGCCGTGCACGCCGNN  
GCCGGGGCGGGAATCT (SEQ ID NO. 252)

## Clone Rv237

::::::::::Rv237SP6.seq::::::::::  
CTCAAGCTTCAGNCNTCTAAGCGGTCTGCGCGGCGATCGCAAAGATCGCCCTTGGCCGGCGTTGGGGGCTTCTGCTC  
GGGGGTGTTGTACACCTTCTCGAACACCTCGGCACCGACACCACCGTCGGCTTGAACACCGCCAACATCGGCAGC



ANATCTTGATGTCCTGGTGAATCCACGGTGACTTTGGAGTGGAAGGCGGCCATACTGATCGCGCGCGCCACCACATGA  
GCTAGCGGCAGGAAAACCAGCAGCCGCTCACCCTTGCGCAGCAGCGTCGGGTGATATGCCTGGCGCCC

:(SEQ ID NO. 253)  
:Rv237T7.seq:AGTCGAANGTCAGTCCGGTCTCCTCTCCGACTACGGCCAAGAACTGGGGCGACGGTGTCTAGTGCAGAACAGCGGAAAC  
TGGTGGCGCCCTAGGCGAGCGAACGCTCACAACGGCGGTGACCGCTTCTGGTCTGCACCATCGAGCCGTGCCAGC  
CCGGCCGCGTGCCGTGACCCGATCCACTGGATGCCCTTCTCGGCGGTTTCAATCANGTACAGGCGACGTTCCGCCACC  
ATCGTGCCGGGCGACGGTAGCGAGAAACGCCGACTTCACCGATTGCCTCGGTGATGxxxxx (SEQ ID NO. 254)

Clone Rv23

:Rv23T7.seq:AGCTTCGCGGCGTGGCGATCGCGGTTCAAGGCGCGCTCTTCGAGCACAACGAGCGAAGACAGCTCGGCGACGGAGCCT  
TTATCGACATCCGTTCCGGGCTGGCTGACCGGCGGCGAAGAACTGCTGGACGCGTTGTTGTCTGACGGTGCCGTGGCGAG  
CCGAGCGCCGTGAGATGTNCGACCGGGTGGTCGATGTGCCGCGGCTGGTGAATTTTACGACCTGACCATCGAAGATC  
CGCCGATCCGCGAGCTGGCGCGGATGCGCCGGCGGCTCAACGACATCTACGGCGGCGAAGTGGGTGAGCCCTTCACCA  
CCGCCGGGCTGTGCTACTACCGCGACGGCTCTGACAGCGTCGCTGGCATGGCGACACCATTGGTCCGCGGCGAGCACTG  
AGGACACTATGGTGGCGATCGTCAGCCTCGGCGCCACCCGCGTCTTCGCGCTGCGGCCGCGTG (SEQ ID NO. 255)

Clone Rv240

:Rv240SP6.seq:AGCTTCAGCTGATACTCGACCAGCCCCACTCGGGCCAATACGTGAATGTCTAGCATCTTCACCCGTTACGGGGCTANT  
CGAGTAGTAGACATTGATTAGCCTGAACGTACCTCCGACGCCAGCTGACGAACGGGTATGACGGATGGATTTCTGTGGT  
GTCGCGCCCCGAGGTCAATTCTGTTACGGATGTATCTCGGGGCCGATGTTGGCGGCCGCGGCGGCGCTGG  
GACGGACTATCCGACGAAGTGGCGGTGGCGGCGTCTGTGGTTTGGGTGCGTGACCTCGGGCTGGCGGATGCGGCGTG  
CGCGGCCCGCGGCGGTTGCGATGGCNCGCGCGGT (SEQ ID NO. 256)

:Rv240T7.seq:CTGGTCATGGACGTTGCTCCGGTAGTGGCTCACTGCCGATCCTCCTCGTTGAGAGTGCCACCTCAGGGTTGGGTAGGG  
TTGGGTACTCGAAACCAAGTTACCCACCAGTAACACCGTCAAAATATATCCGTTGCATAGGTCAATGCAAGTTGATGT  
GAGCTACATTGCACCAACTAATAACCAACCGGTTGGGTTAGCGGTGATCCTGGCCGTGTCGGTCTCTCACCTGCGG  
TGATAGCGATCAAATGAAGAATATGCGGAGTCTAGGGCGGCGAGCGCCTGGCANCCTAGATCATCGGCTCACGCGGATG  
CGGCCTCTTGGTACGGACATGCGCGCG (SEQ ID NO. 257)

Clone Rv241

:Rv241SP6.seq:CTCGTGAGTAGCACCCCTGTAATTTGGGATCGGCAAAAAGGCGAATCACCGCGTGGCCACGACACGCCGGGAGGGACN  
ATCTCGGGCGGCTAGGGCTTCTCGCGGGAAGGCCCGAAGCTACGGCGTTTCAACACGTGCGCGTCCGCCCTCCGACCGCG  
AACATTCCGGGATGGCAGCAACCTGG (SEQ ID NO. 258)

:Rv241T7.seq:GGATCAACTACCGGCCAACGGTGATTCTTGGGCGCCGCTGACGCGCGAACGACCCAGCGACACATTACGAGATGGCC  
AGCGCGTGCCGGGCCACGATGTTGGTGTCTCGGCGGCTACTCCCATGGTGGCGCNCGTGATCGACATCGTCACCGCCG  
ACCACTGCCGCGCTCGGTTACGCGAGCCGTTGCCGCCCGCAGCGGACGATCACATC (SEQ ID NO. 259)

Clone Rv243

:Rv243SP6.seq:AGGACCGTCAGCACGGCGACGTGCTACTCGCCGAGCAGTGGAATCGCTCTGCAGCAAACCATTAATCTGCGCGACGT  
TCGAGATGACCTTCTGAATGGACGGATCTACCTGCCGCGGACGACCTGGACCGCGTATGCGTCCGCCTCCGCCTGGA  
CGACACCGGGCACTCTATGACCCCGACGGACGGCTCGCGGTACTGCTGCGGTTACCCGCCGACGCCCGCACGGTACG  
CGTCGGGACTGCGCTGAGTCCANCCTCGACGCCGTAGCGCTGCTGTGCGGCCATGTCTGGCATCTACCGCCGTCG  
CTCCCTGA (SEQ ID NO. 260)

:Rv243T7.seq:CGACTCTGTGGCCACTGCGGGTCGATCTTGCGGCCGCCCGGTCGTGGAACGCCAGGTCACCCGGCGGCGCACCGC  
GGTCAGCGCGTCGTTGGCCAGCGTGGTCACATGGAAGTGGTCGACGACGAGCTTGGCGTTGGGCGAGAGCCCGGGCGT  
GCGGATCGCCGAGGCGTATGACGCGGCGGGTTCGATGGCCACCGTACTGGATGCTCTCCCGGAAGTGGGTGTGCGCG  
CTTGACCCATGCCAGACCGCCGCGCCGCCGCGGCTTCATGCTGCCATAAACCTGATACCGGCCAGGTGACNA  
ACCNGTATCCACGGTCAACCC (SEQ ID NO. 261)

## Clone Rv244

.....Rv244SP6.seq.....  
CACACGGACGGCGGTGCGGACGCAGCTGACGCGCATGGTGGTCTAGCATCGCGGCCGGTCTGCTGTTGTATGCCTACTT  
CGCGCCGCGCAAATGCTGGTGGGCGGCGGTGGTGGCGCTCGCATGGCTGGGCTGGGTGCTGACCCAACCTCTCGAACCA  
CACCGGTGGGTGGGCTGGGCTATGGCCTGCCATATCGGCCCTGGTGTCTACN (SEQ ID NO. 262)

.....Rv244T7.seq.....  
CCGATATCCGAGCCGATAGCTGGCGGGCTCGGGTGGTNGCCAGCGGCGCTGCGACGAAAGTGTGACCGTCATGAAACA  
GACACCACGGCGGCCGTCGGCCGTCGTCACTGCTCGAGATCTCAGCATCCGCGAGCCGGTGTGATCGCGCTTTTCGGC  
GTGTAGTGGGTGCGCGCCGAGCCCGCAAACGCCGGCCGACACAACCCCGGAACAGGAAGTCCGGTCACCGCGCC  
(SEQ ID NO. 263)

## Clone Rv245

.....Rv245SP6.seq.....  
GCTTCAGGACAAATTGNATCCCTATGCACCCGTTGTACGCCGATGAGTGAAGACTGCACGCAATCGCCGGAATCCGG  
CAAAACCCTGCACAAGCGAAATCAACCGGAGGCTGACAAGGCAACGTCGGTGATCCGTACCGCCTGGTTGGACAAACG  
GCAGAAGGCGCCTCGTCCGGTCCATCTACGCCGAGCACACTGGTGATAGCGCCATCGGCATCGGTGCGGCCACGGTGG  
AGACGAACGTCGCGNGCGTCTGGGTGAGTAACCCGCCGACCAGTTCTCGGGCAAGCTGGTCAACATCGGGCGCCACG  
TCTCCAAC (SEQ ID NO. 264)

.....Rv245T7.seq.....  
GTTTGGCGGCCCTTATGCACTGAGGTGCTCAATTGACCCACAGCGGAAATGCCGACTATTCGAGGCCCTCCTTCGCCT  
TGGCTGCCGGAGATGGGCTCCGCGGGAACCGCATGCAGGTATATGACCTCGGTTTCTCGGGTGTACCGCGTGCCTTG  
TCGAGGATGAACTCGGCGTTGGAATTGTCCAGCCGGCCCAATTCATCGAGCGCAGATTCGTACACATGGCGCGCGCG  
ACATACCTTCACCGTGATCTGCTCCACACGGACCGCCTGTGCGGATCTGCTCACGGGTAAAGGAATTA  
(SEQ ID NO. 265)

## Clone Rv246

.....Rv246SP6.seq.....  
GCGCACTCCTCCTTATCGCTCCGCTCTGCATCGTCGCGGCGCGGTGAGGTGCAAACGCCTTCGGGGGTGGGGTCTTG  
CGGAGCACACCGGATACGGAGCGCAACGCGTCGCGTTGTGCGGGCAAACAAGTGTGACGNNCCAATGCCATGTCCAG  
CAGCTTATCAGTGTCGAACGTGCGAACGTGCGCCCTTCGCCGGTGCCTGAATCTCTACAAG (SEQ ID NO. 266)

.....Rv246T7.seq.....  
CGCTGAAAGCCACCATTCGCGGGTTCGGGCGCCGGGCTCGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCG  
CGACACCACCGGCTGCGCTACGTGAGCCATACCGGGCGGAGCTACATCGGCTCGGCCGCTAGTGTTTCGGGNCCTC  
TTTCGAGGTGAGGTGCA (SEQ ID NO. 267)

## Clone Rv247

.....Rv247SP6.seq.....  
TGTAATTTGGGATGGGCAAAAAGCAAANCACCGCGTGGCCACAAACGCGGGGAGGGACAATCTCGGGCGGCTAGGGCT  
TCTCGCGGGAAGCCCGAAACGTACGGCGTTTCAACACGTGCGCTCGCCTCCGACGCGAAATTCGGG (SEQ ID NO. 268)

.....Rv247T7.seq.....  
CTTGGGCAACATGCTGAGGATCGCCTTTTCAACACGCGGTTCGGGGTGGCGTTGCATTAGCTCACCGATGGTGCGCTTG  
TTGCAGGCCCGCGGATACCCGAGTGCCGGTAAACCATCTTGTGCTGCAGTTTGTCCCGCTGAATGGCGACCTTGTGCG  
GTTGATCACGATGACGAAGTCACCGCCATCGACATTGGGGGCGAACTCGGCTTGTGCTTG (SEQ ID NO. 269)

## Clone Rv249

.....Rv249SP6.seq.....  
GCATGCTTCATTATCTAATCTCCAGCGTGGTTAATCAGACGATCGAAAATTCATGCAGACGGTCCCAAATAGAAAG  
ACATTCTCCAGGCACCAAGTTGAAGAGGTTGATCAATGGTCTGTTCAAAAACAAGTTCTCATCCGGATTGAACCTTACC  
AACTTCATCCGTTTCATGTACAACATTTTGAANCATGCTTC (SEQ ID NO. 270)

## Clone Rv24

.....Rv24SP6.seq.....  
ATACTCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACCACGCGCGGGTTCGGGCGCGGGCCCGG  
GCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCGGCTGCGCTACGTCTATCCATACCGGGCG  
GAGCTACATCGGCTCGGCCGCCCATTTGTCNGGCCCTCTTTCGAGGTGAGGTTATACCGATTGGGCATCGG  
(SEQ ID NO. 271)

.....Rv24T7.seq:.....  
TCCGTACTGGTCGGGTACGCTTCGGTTCGAGTGTGCGAGTGATAGATGACGACCGGGACCTCGTCGGCATCTTCCATA  
GCCCCGCACACCTTCAGTTGCTCACCAGGAATCCAAACGGTAGAAGGTGCGCGAGCGCTCGGCATTGGTCATCGGGATA  
TGCCGCTCGGGACGGTCAGAACCTCGGGTCCG (SEQ ID NO. 272)

## Clone Rv251

.....Rv251SP6.seq:.....  
GTTCTCGCACGATTTTCGGATTAGCGGGATGGTCTCAATTGGGTATGCGGGGAAGGCGCTGACATTCGCCGCGATTAGC  
TGTTTGATGGACCGGGGTGATTTTTGATCACGGAATGGGTGTTTATNCAGGTCGCACGCTTTCATCCGGGGCGGAA  
CG (SEQ ID NO. 273)

.....Rv251T7.seq:.....  
GGGTGTGCCTGCTGTGTATGCACGGCATAACGGACATCCTTCCCCTGAAGACCCGCGGTGGAACAGCCACGTGTCCATC  
ATCANGGGGTCAACCCCGGCCAAGGGCGACGGCACGCCAAGTTGCGCGACCGTTAACCTAGTGCTGTTAGCTTCATTT  
GCTGCGAGCAAAACAGCTGGTCCGNCGTAGGAATGAATTGAACTCAACCGATTGGTGCCGCCGTAGGTGTCTGG  
CTG (SEQ ID NO. 274)

## Clone Rv252

.....Rv252T7.seq:.....  
ACTACCGGCCAACGGTGATNTCTTGGCCGCCGCTGACNGCGGAACGACGCCAGCGACCACATTCAGCAGATGGCCA  
GCGCGTGCCGGGCCACGANGTTGGTGTCTCGGCGGCTACTCCCANGGTGCGGNCGTGATCGACATCNTCACCGCCGCAC  
CACTGCCCGGCTCGGGTTCACAGCCGTTGCCGCCCCGAGCGGACGATCACATCGCTTTTATTNNNTNTTCNGGAAT  
CCCTCGGGCCGCGCTGGCGGGCTGATGA (SEQ ID NO. 275)

## Clone Rv253

.....Rv253SP6.seq:.....  
ACGTCGGGANACTGTTTCGCTTCATCCTCGTCTCGGCGGATTGGTCTGCTGCGCCGACCGACCGATCTTCAGCGGGG  
GGTCACGCTCCGTGGGGTGCCGTACTTCCGATCGCCAGTGTGCGCGTGTGTGGCTGATGCTGAACCTCACCGCGT  
TGANTTGGATCGGTTCCGGATCTGGCTGGTGGCCGGAACGCNATTTATGTCGCTACGGGCGCCGGC (SEQ ID NO. 276)

.....Rv253T7.seq:.....  
GCTCAAAGGCACTACTGGCACCAAGGCCACACGTACCTGTGACTCCTGCGCCGACCCGCCGAGGTCTGGCCGTTA  
CACCAGACGGGCGAGCCGGGAGTTGGTACCATCGAACAAGACAAGGTGCATGGGCGGAGTTGTTCCGCCACTTCGTGC  
ATGACGGGTC (SEQ ID NO. 277)

## Clone Rv254

.....Rv254SP6.seq:.....  
CGATACCGGCTGCTTACCGAGACATCCACCATGCCACCCGAATCACCGCACGCGCCGAAATCGCACAAACAGCTTGACG  
CCTTGACGGTTCGCGGATTGGAATTGCCGACGGTCTCTGACGGCGTCGACCTTGGCAGCCTCTACGAGCTCTCGGAAT  
CACTTGCCCAGCAGGGGGTTCGATGAGTGTACACCCGAAGACCTCGATATGGGCGCAATCCTGGCCGACACATCCAAC  
CGGGTGGTTGTGTGCTGCGGCGCCGGTGGGGTCNGCAANACACTACCAGCGCCGCGCTGGCGTTGCGCGCGGCCGAAT  
ATGCCCCACTGTGGTCG (SEQ ID NO. 278)

.....Rv254T7.seq:.....  
CGTCGTCGTCGTTGGTATGCGATAGCCATCCCGTCGGGCTACTCGCCATCACCGATCAGCTTCGCCCCGAAGCCGCGC  
GGCGATTTCCGCTGCGACCAAACAGCCGGGGCCAAACGGTATTGCTTACCGGCGACAACCGGGCCACCGCCGATCG  
GCTCGGTGTACANGTTGGCATCGACGACGTACGGGCGGGCTACTGCCGACGACAANGTCGAGCCGTGCNGCNGCTG  
CAAGCTGGAGGTGCCAGATTGACCGTGGTGGTGACGGTATCAACGACCTCCGGCCTTAGCGGCCGCGCATGTGCGCAT  
CGCCATGGGCGAGCGCCCGAC (SEQ ID NO. 279)

## Clone Rv255

.....Rv255SP6.seq:.....  
GCACGCAATCGAAGTCACCCAAACCGGGCGGGCCAGGCGTCTNACGCCACGTGNACCAGCCGCAACCTCAACCCGGCC  
ACGGCGAGCTCCTGATCAAGGCCGAGGCCATCGGTGTCTACTTCAATCGACACCTACTTCCGCTCCGGGCAATATCCG  
CGCAACTCCCGTTCGTCTCTGCTCCGAAGTATGCGGCACGGTGGANGCCGTGCGCCAGGGGTTAC

(SEQ ID NO. 280)

.....Rv255T7.seq.....  
TCGACTGTGTGGCCACAGATCACGCCCCGATGCCGAGCACGAGAAATGCGTCGAATTCGCCGCGGGCCGGCCGGCAT  
GCTCGGGTTGCAGACGGCATTGTCTGGTGGTGGTCATACAATGGTGGCGCCGGCTTGTGTANTTNGGCGCGATATCGC  
CGGGGTGATGAGTGANAACCGCGTGCA (SEQ ID NO. 281)

Clone Rv257

.....Rv257SP6.seq.....  
GAACCTGACACCCCTGGTCACGGGTGAGCACGGACTTGATTTCTTCNCTATTGGTGGCGCTGTTGAGCACACCACGCC  
GCTGACGGCCGTGCGCTCCTCGCTGTGCTCGGTCTGGTGGAGCGCGCTGCCCGCGCCNAACATCNTAAATCAAGCGT  
ATTCTGCAACAGATATCATCAATGTCGGCGCTGGACTATTCAAATCATCGATATACTGGTGACCTGGTCCCTCGCCAT  
CGATCAATGGCGATAGTCACGCAAATCGTCACGGACATCGTCGGCGTCCAGCTGGCCCCGTGCCAACAGATGCTGCAA  
CCCATCGGGGTGGTATCACCGCGGTGCTCGGCGATGGTCCACAATTCTTGGGTCCAAGCCCNAAACATCCCGGGCAT  
GAATTCACCGGCATGCGCN (SEQ ID NO. 282)

.....Rv257T7.seq.....  
CTATCGTACCCGCGCCGGTCACCTTCTGGATATCGCCGGCCTGGTCAAGGGGGCGTCCGAGGGAGCCGGGCTGGGTNA  
CAAGTTCTTGGCTCATATCCGCGAATGCGACGCCATTTGTGAGGTGGTGGGGTGTTCGTGACGACGACGTGACTCA  
TGTACCCGGACGGGTGATCCCCAGTCCGACATTGAGGTGCTCGAGACCAGCTGATCCTGGCAGATCTGCAAACCCCT  
GGAGCGGGCCACGGGCGGGCTGGAGAATGAAGCGCGCACCAACAAGGCGCGCAAGCCGGTCTACGAAGCGGCACTGCG  
TGCCAGCANGTGCTCGACGCCGGGCAAGACGCTGTTCCGCCGCGGGGTGGATGCCGCGCGCTTGCAGACTGAAACT  
GCTGACCACCAAGCCCTTCTGT (SEQ ID NO. 283)

Clone Rv258

.....Rv258SP6.seq.....  
TACTCAAGCTTCAGGCCGCCACGTCCGCCGTCCGTGCGCGACGTGACCTCGAGCGCCGAGTTCGACTCGACATCGCCG  
CCGGCGCATGCCGACATGAACGCGGCACTCACCGCAAGCCCGTCGGACGTGAGGTGATCGACTCCGCTTCAAGCACCC  
GGATCGTCCGGGCAACTCGCGGCTCGGCTGTGCGAACGGCACACCCGTGCTGGCGGCNCCCCGCGCGGAAGTGGGC  
TCATCACGGTCTTGGAGCCGGTGCCTCACCGGTACCGACGCCGTC (SEQ ID NO. 284)

.....Rv258T7.seq.....  
CCGACATCGAGTGGGCTCGCAGTGACTTGGCGACCTCCAAGCCACCGGTACCCGCCGCGCGGCAAGCCAAGGACGACG  
ACGGCCTTGCCGATAGCTGCGCCAGGCGTTGCGCCAACTGGCGTCCAGCGTCGCCACGATCGTCAAAGAGCTTCATC  
TGCCGAGTGTGTCGCCATCTCATGGCTCCAAATATGGAATTAGGTCCCTGGGCGGACTGACGACAGTCCCTCAGCGAC  
CGGATTGCGCATCCCGCCTTGTACGCTACTCCGCAAATCCCGGGCTTGGTCCGCGGAAGCGAACTCGGCGGCGCTAC  
GTGGTGGTTCACTTCGGCCGTGCGCACTCGGATCGACGGGCCGATGGTGGCCGGGCCCGCGCTTCTTGGTCATCCG  
ATTGAGT. (SEQ ID NO. 285)

Clone Rv259

.....Rv259SP6.seq.....  
ATACTCAAGCTTGTGCGGGTAAACCGCACGAGGGCGGTGGGTGCGGTGTCAAAGACACCCACACTTCTTTGCGGTTTC  
GGTGATCTCGACACCGGCCGCGAGCCGACCACCATGCGCGCGTAGATCGGCGATCAGCGCGTGGCTATCGCCTGGGT  
GCCGCCACCGGAATCGGCCAGCCGACCGAATGGGCCAGCGTTGCCAGCATCAGTCCGGCGCCGGCCGACACCACTGA  
CGGCAACGGTGAAATCGCGTGGGCGGCAACGCCGGTGAACAACGCGCGGCATCCTCGCCGCCAACGACCGCCAGGC  
AGGGTGCTGGGCCATCATCCGACGCCGA (SEQ ID NO. 286)

.....Rv259T7.seq.....  
TGGACTCATAACGATCGGGTCAGCGACGCGCCACACGAACGGCCGGACGAGTGGGCCAGGGTCGCGCCTCCCCTACA  
AACAGGATCCGTTGCCTGCGAGCGACAGGCTCCGGTGGCGCGTGGGCGCCGTGCTCGTCCAGCGTCCGGTCCCGGG  
TCGCCGGCGACGCTTGTTCCTCCATACTCGCCCCCTAATCTCGAGGACGCCGTACCCGAGGCAACCTCCCAAAA  
TGCAATCCCCAAAATGCAATGCGTCGAGCTATTCTCACACCGACCGTAGTTGCGGATCAGAAATCCGTTGGGCGC  
GGAAGTCCAGCCGAATTTGTTCTCCCGCTCCGCATCATGCTTGTAAATCGTTTGGAAATCATCTCATATGCCTCGATC  
GCTTCATAGGTCAAGCCCAACCCGGCAGGATGGGTGGCC (SEQ ID NO. 287)

Clone Rv25

.....Rv25SP6.seq.....  
CTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATG  
ACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTAGTGGTTGCGCACGTAAATTCGTGAGGT  
GACCGATCCCTGCTGTCTCACTCGCCTCACAGCGACCAACACGGCTGGCGCTCAAGGCGGGCACGTGCGGAGCAGAT

GAGGAATGTGCGACGTCTTGATGCAGCCTGTGAGAACACCGAGACCCTCGACGAACCTTACGATCGAAACCGCTTAGGC  
CAACCGGTGACGGGGGTGTCTTCCGCGGCTAGGCGCCTTATCGTCCGAAGGCCGTGGGTGGTGATCGCCTTCTGGG  
TCGCGCTTGCGGGTCTGCTTGCGCCGACGGTGCCGTCCCTGGACCGATCTCCAGCGGCATCCAGTGGCGATTCTGCC  
ATCGG (SEQ ID NO. 288)

.....Rv25T7.seq:.....  
CAGGCATGCAAGCTTGCGATGTATCAACACGCCGTTGCGCAGCGTGAGCCGATAGTTGACATCCGGCTCGGTGAAGGT  
GAAATCGATGGCCAGGTGAGGTCCCATGCGCGTGGGCCATTGATGCTGATCGCCAGGACGTCAAAGATTGGTCCGG  
CGTCAGCTGGGCGAAAAACGTGGGCGCCGGGACTTGCCCGGAGCTGCCCGGTTCCTCGCGCAGCTCGGCGGCCCC  
GGTCAGAAAGAAATTGCGCCAGGTGCGACACTCCGCGCCGTAGGCCAGCTGCTCCACGGTGTGGCGATATAGCCCCG  
GGCCGACGCTGCTCGCTGTCGGCGAACACCGCATGGTCGAGAAGCGTTGCCGCCAACGGAAATCACTGCGTCAAAG  
CTTCGCCGGGCCACTCCAGCACTCCGTC (SEQ ID NO. 289)

Clone Rv260

.....Rv260SP6.seq:.....  
ATACTCAAGCTTGACCGACGTGATCGCACCACGCGGGAACCTCAAGGGCACTACTGGCACAAGGGCCCCACACGTC  
AACCTGTAACTCCTGCGCCGACCCCGGCCGAAGTCCTTGGCGTTAACACCGAACGGGCCAACCCGGGAATTGGGT  
CCATCAAAACAAATAGCAGGTGCTTGGGCGGAGTGTT (SEQ ID NO. 290)

.....Rv260T7.seq:.....  
GTCGTGCTGTGCTGGGGCGTCCGTATCAGCACGCCACGAAATGGGGCACAAGAAGGATTCTTGAACGGTGGCTGTC  
CAAGATCACCTCGCCCAAACTGCTACGGGCACTTCTACATCGAGCACAACCGTGGCCATCACGTCCGCGGTGTCCA  
CACCGGGAGG (SEQ ID NO. 291)

Clone Rv261

.....Rv261SP6w.seq:.....  
ATATGCCTTGCTGAGCTTTTCGGATCGCAGCGAGTCGTACCCGCGCCGGTCACCTTCGTGGATATCGCCGGCCTGGTC  
AAGGGGGCGTCCGAGGGGAGCCGGGCTGGGTAAACAAGTTCTGGCTCATATCCGCGAATGCGACGCCATTTGTCAGGTG  
GTGCGGGTGTTCGTGACACGACGTGACTCATGTACCCGACGGGTGATCCCCAGTCCGACATTGAGGTGCTGCGAG  
ACCGAGCTGATCCTGGCAGATCTGCAAGCCCTGGAGCGGGCCACGGGGCGGCTNGAA (SEQ ID NO. 292)

.....Rv261T7.seq:.....  
GACACCCTGGTCACGGGTGAGCAGGACTCGATTTCTTCGCTATTGGTTCGGCGCTGTTGAGGCACAGCACGCCGCTGAG  
GCCGTGCGCTCCTCGCTGTGCTCGGTCTGGTGGAGCGCGCTGCCCGCGGCCGAACATCGTAAATCAAGCGTATTCTGTC  
AACAGATATCATCAATGTCGGCGCTGGACTATTCAAATCATCGATATACTGGTGACCTGGTCTTCGCCATCGATCAA  
TGGCGATAGTCACGCAGATCGTCACGGACATCGTCTGCGTCCCAGCTGGCCCGTGGCAACAGATGCTGCAACCCATCG  
GGTGGTATCNCGGGTGCTCGGCGATGGTCCAACAATTCTTGGCGTCCAAGCCCGAAACCATCCGGCCATGAGTTC  
ACCGCATGGCGCAACGGCTGGTGCCGGGCAAAACGCGCGCGATCGAATTC (SEQ ID NO. 293)

Clone Rv262

.....Rv262SP6.seq:.....  
TGTAGAAGGTGGGTCCCGTCCAATTCGCGGGCGGCGCGGATATGCCTTGCTGGTCTTGCTCATTGATATCCAATC  
TATGGGTCTGTTACTCAACGGGCCGAAGCTGGCCCTCCACGGGTAGGTCCTATTCGACGGTGATGTCC  
(SEQ ID NO. 294)

.....Rv262T7.seq:.....  
CCCGAATCCGGTGGCCGGCAGGGGGCCTGGCGACGTGGACACCTTCTAACTTGTCTTTACCGGTCACTGTTGCACCCC  
AACACCTTTAACGACGTGGACGGACGTTACATCGGATTGACGGTGTATCCACAGCGTTGCCATTGGGCACACCCAC  
TACGCCAATTTCTCCGACTGGGACACCTACCGCAGCTCGCCCCACTGCAGGGACTGTTGTTCCCGCAACGGGCCATC  
GACATGATCCAGTCGTTGGTGACCGACGCGGAGCAGACTGGTGCGTATCCGCGTTGGGCGCTGGCGAAATTCCGCCAC  
CGGCATGAT (SEQ ID NO. 295)

Clone Rv263

.....Rv263SP6.seq:.....  
TTGAGATGCTGGTGGGATGCCGATGGTTGGAACATGGTCCCCTGGCGTCGAATACGCGCGAGCGCATGAGCTCACCG  
GTTCCGAACAACGTATCGAAGAATCGCACTGCTGGCAGATGGTATCTCCGATGTGGTTGTAATTTGTATCCCAACTC  
TAACTGTGCTATCGGATCTGCGTGAATA (SEQ ID NO. 296)

.....Rv263T7.seq:.....  
CGTAATCACGATCCCGCTGAGACACTTGACCTTACGGCCGAAGTGACTTCGCTGCTGCTATGCCGACACCCGATTTCC  
ATACGCTGCTGTACACGACGGCCGGCCGGTGGCCTCCATCACGCTCAACCGCCCGGAACAGCTCAACACCATCGTCC  
CGCCCATGCCGACGAGATCGAGGCCGCTATCGGGTTGGTGAACCGCACCAGGACATCAAGGTCATCNTNCTGCGCG  
GTGGCGGGCGCGCCTTCTCCGGCGG (SEQ ID NO. 297)

## Clone Rv264

.....Rv264SP6.seq:.....  
CAAGCTTAAGCTGGTCCGGCACTCCATGAGCCGTAGTGCAATGGTTCGTGCACGGCGAGGCCGAAGTTGCCATAAA  
CATCCCTGACGAAAGTCTCCGGCAAGCCGATTGCTTCTTCGGGCCGCTTCTTGTGGATTGTCCGATAACCCGGTCCCT  
CATGCTGGAAGTTGTGCGCACTCTTCTTCCGCGATGTGGGCTAACGACTCGTCATTGAGCAAGAAGTACGTGCACA  
GGCATCGTCCGCCGGGCTTCAGCACGCGGGAGATCTCGTCCAGATAGTGCTCCACGTCCGGNGGGAACATGTGGGTG  
AACACCGAGGTNAGAAACACCNCATCCAACGACGCATCCGGGATATGGAAAGCGAAA (SEQ ID NO. 298)

.....Rv264T7.seq:.....  
TATGGTCTTCGTGACCACTACGTGCTAGGCGCCATGAGCCAGCGACTGAAGCCGCGCCATGCCTGCACGGCCCGCTC  
ATCCAGCGAGGCGGCCATCTCCCGCAGATAGCCTGCCGCTCGGGCGCGACGCTGTCCGGATCGCGTCCGAGCTCGTC  
GGCCAGCGCACGACGCGCTCGTCATACCATCGGGCATCCAGCAGTTGGGTAACTCAACGGGGTCCGTGCTAGCGG  
CGTCATTGATTAGCAACAATACCGATGCGCTGCAGCAACTTTCGAGTCCGATGCGGCCACCTCCCGTGCAGTCAC  
TGGCTAGCCCCGTCATGCCGTTGTGTGATGGCACGGCAGCGGGCTCGTAACTGCGGTCTCAGCTCGCTGG  
(SEQ ID NO. 299)

## Clone Rv265

.....Rv265SP6.seq:.....  
GCTTAGCGGTCTTGCTCGAACCGACATTGCGTGCCACTCATGAGCGGGTGGCGGTGCGGTGCTTACACATCT  
(SEQ ID NO. 300)

.....Rv265T7.seq:.....  
GTATCTGGCGCTCTCGAATATCCTTGAACGTCCCGGGTGCCACCCAGATAGATCGCAGCGCCCTGCAATGGAGTTC  
CCTTTATGGCCTCTCTAGCCTCCCGCTTGATCGGCTCGACCCGAGAGATGCCCTCGGGCGTTGCGGGATCTCCCTCCA  
(SEQ ID NO. 301)

## Clone Rv266

.....Rv266SP6.seq:.....  
CTTCACGCCGATCCGCGACCGCGAAGCGGACGGTGACGGTGGGCGACAAGGTTCCGGTTGGTCCGCCGGCGCTGGGCG  
ATATCAGCTCACCCGGTTTCGAGGTGTTCCGGCACCAGGACGGTGCTGCAGACATTCTTGAGCGTCTCGACCGGCCCG  
ATTCGGCCTTCAACATCGTGACGCCGATTTCGGCGGTACCGCTCGGCGCCGAGTCGAAGGCGGCTGAGCTAAAGCC  
GGGCAATTGGCGGAGTGGTAAACAAGTTCGGTGACTTCGGTTGACCGACTCGACGGGCTCGATCTGGGCGCGCTGGACC  
GGTATCTGCGTTCGCTGGGGATCGGGCCNACCGCNANTTGCCTTGCGANCTGATTCCGGTGGAGCTCCAATCTGACTT  
CCGG (SEQ ID NO. 302)

.....Rv266T7.seq:.....  
GCAGCTACCGACCCTAGCGACGAGTGTTTCGACGCTCGAATGTGAACGTTCCGGCTGATTCCGGCGCGGGTTCCC  
GCTCTCAGCGCACGTTCCGGCGCGAGGNGGCTAGTCCCTGGTTAAGCAATGTCTCGGTCCGCCAGCAGCGCGCATG  
TCGCCAACCCGTCNACCGGTTGCGCATGTCCGGTACCGACGGAACGACGGCGCGATCCGGATGTTCTTGTGCTCCG  
GATCCTTTTCGATACGGGAACGACCCCCCGCTCGGTACCGCGATACCAACGTCCTTAGCCAANGCTACNGTCCGGCG  
CGCGGTCCCGGCAACACGTCGAAGCTGATGAANTAACCACCCTTGGGCTCGGTCCAAGANGCGATCTTGACTCCTT  
AACCGCTGATNCAA (SEQ ID NO. 303)

## Clone Rv267

.....Rv267IS1081N60.seq:.....  
TCCCCATCGGCGCCGGACCGTTTGAAAGTCCAAGCACGGGTGGGATGGAATCGACGACAGTTGAGCGCCGTCGGTGGC  
CGTGGTACGAGCTGTTTCGCGAACGCACCAAGGTACATCCCTTCGACATCTCACCGACGTGGCACGGGCGACATCAAC  
AGGAAGATTGACGAATCCCTCGCAGGCGCGGACGTCGCGAGGCCAACGCCAATACGGGGCCACCAGCGATCCTCCG  
CTCACGCACGACCCCAAGCCAGGCTCANCCACCCAAGTGGGCCCGGCTCTCCCTCGCCCCCTGGTCTCCGGGGCCTT  
GTTAAACAACTACCGGAAGTCCACCAATCCTCGCTGCATCTCGACACCGTCCGCCCTCACTCCCTTCTCCGCCCCCTC  
TCCACACNACACACTCTTGCAATTAAGTTCACGGAGCGGTCACTTTTCGTGCGACGAAATTCGCAATCCGGCCGCTCG  
CCGCCAGAGAT (SEQ ID NO. 304)

.....Rv267SP6.seq:.....

CGGAAAGTGGATAC TCCAGCAGGTAGCAGGTGCGCCACCACGCTGGTCAGTGCGCGTTTCAGCTCGCTTGCGGCGCTGC  
AGCAGCCAGTCCGGGAAATAGCTGCCCTGGCGCAGCTTGGGGATCGCGACGTCGATGGTTGCGGCACGGGTGTCGCAA  
ATCACGGTGGCGGTAGCCGTTGCGCTGATTGGACCGCTCATCGCTGCGTTTCGCGGTAGCCCCCCCCGCACAGGGCGTC  
GGCTTCAGCCCCCATCAAGGCGGCGA (SEQ ID NO. 305)

.....Rv267T7.seq:.....  
GGCCGAGTCCAGCACTTCGCACTATGTGCAGACCAANACCCGGTGGTTCGCCGCGCTGCGGCAGCGGCTGGCAACGGC  
GCCGGTGATCACCGAGTGGTGCNAGTTGCCGACCGGCAGTTCGCCGCGGGCTTACTACGAGAAGGGCTGCGCGACG  
TCATCAGGTATCACGTGTCGATGACGTCGAGCGTTAACTTCCCCGACCAGACGGCGACCTCGCCGATGGACCCCGCGT  
TGTACCTGGTGTGGGCGCAAGCTAACGCCGCGCANGCTATCGGTACTCGGTCGAAGCGCAGCCGGGGTTCGCAAGCGC  
TAGCGGGCAAGGTCGCGACGATCTCGGTACCTGGACCAACTACGGCGCTGCTGCCGCCACCGAATAGTGNGTGCCCG  
GCTACCGGCTGGTGGATTCCACGGGACATGTGGTTCGGACCTGCCGGCAGCGGTGGAAGTGAAGANGCTGGTCT

(SEQ ID NO. 306)

Clone Rv268

.....Rv268SP6.seq:.....  
AGCTTCAAGGACATCGTCATCGCGACCAAAACCGCGAGTAGGTGCGGCATCCGGGAAGCATCGCGACACCGTGGCGCC  
GAGCGCCGCTGCCGGCAGCCGATTAGGCGGGCAGATTAGCCCCGCCGCGGCTCCCGGCTCCGATTACGGCGCCCCGAA  
TGGCGTCACCGGCTGGTAACACGCTTGC CGCGCTGGGCGGCGGCTGCCGGATCAGGTGGTATATGCCGACAAAGCC  
TGCGTGATCGGTATCACCAACGGTGACAGCAGCCGTTGTGCACCATCGCNAACGCCACCCCGGTCTCCGGGTCTGT  
CAN (SEQ ID NO. 307)

.....Rv268T7.seq:.....  
GCTCGCGGTCCAGCAGCAGACGTGTCTGACCCCGACGCCCGGCCGCGGTACCGAAACCGGATCGGCCCGCCGATGGC  
CGCGGCCACGGCGTCTGCCTTACCCGGCCCGGATACCGCAGCCACACCTCGCGGGAACGCTGAATCGCCGGCAGGGT  
CAAGGTGATTGGCGGTGGCGGCGGTTTCGCGAATCGTCCACCGCCACCACCATGCGGGTGCTCTCGAAGACGCGGGG  
TGTGCCGGAACAGCGAGTTAATGTGGCCCTCGGGCCCATGCCAGCAGGTGGACGTCGAAATTGCGCCCGGGTCACC  
TGGTGCGGCACTGGCGGCC (SEQ ID NO. 308)

Clone Rv269

.....Rv269SP6.seq:.....  
AGCTTGTGATCGTCCGGCAGCGTCCGGCGAGTCAAGTCGAAGCCAGTCCGGTCTCCTCTCCGACTACGGCCAAGAAC  
TGGGCGACGGTGTGATGCATACCGCGGANACTGGTGGCGCCCTAGGCGAGCGACCGCCTCACAAACGGCGGTGACC  
GCGTTCTGGTCTGTGACCATCGAGCCGTGCCATCCCGGCCGCGTGGCGTCAGCCGCATCCACTGGATGCCCTTCTCG  
GCGGTTTCAATCAGGTACAGGCGACGTTGCCANCATCGTGCCGGGGCANGG (SEQ ID NO. 309)

.....Rv269T7.seq:.....  
TTGGTGATCATCGNCCCAACGACCCCGAGGCGATGTTCTTGCACACCGAGGAGTGTGCGAAGCTGGGGCTGGCCTTCG  
CCGCCGATCCGTCTCAGCAGCTGGCGAAGCTGTGGGGTGAGGAAATTGCGAGGCTCGTCAACGGTGTGCTTACTTG  
TTCACCAACGACTACTAATGGGATCTGCTGCTGTCCAAGACCGGCTGGTCAGANGCCGATGTGATGGCGCAGATCGAC  
CTGCGGGTGACCACATTGGGTCCTAAGGGTGTGATTTGGTAGAACCTGACGCACCACCATCCACGTGCGCGTTGGTC  
CCCGAAACAGCCAGACCGA (SEQ ID NO. 310)

Clone Rv26

.....Rv26SP6.seq:.....  
GGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAGCT  
ATTTAGGTGACACTATAGAATACTCAAGCTTGATTTTGATCATCATGATGATCATCACCCGAAGTGTGGTAGCCGAG  
TGGTTATCGTGGGTACCGTCGTGCTTTCCATGGGCGCCTCTTTCGGGCTTTCCGTATTGGTCTGGCAGGACATTCTGG  
GTATCGAGTTGTACTGGATGGTGTGGCGATGTGCGTGATCCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGC  
TGATTTCCCGGTTGAAAGAGGAAATTGGGGCCGGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGGAG  
TGGTGACGGCTGCCGGCATGGTGTTCGCCGTTACCATGTGTTGTTGTGTTGAGCGATTGCGAATT

(SEQ ID NO. 311)

.....Rv26T7.seq:.....  
CAGGCATGCAAGCTTGGCGTGCCGTTCCAACCCGAATTGGCTTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTC  
AACGACGACGTCCTCCGCGGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTA  
CAACGCCGCGCGGAACGCTTCCGCCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGGGGTGATCGTCGATGAC  
GGCATCGCCACCGGAGCGACGGCCAAGGCGGCGTGCCAGGTGTCGCCGGGCGCACG (SEQ ID NO. 312)

Clone Rv270

.....:Rv270SP6.seq:.....  
GGCATCTTGGCCGCCATGTTAGCCACACTGCCACCGGCTATAGAAGCGATGCGCACCGTCTCTGCCAGCACATTGCGGC  
GCTCCTCCCTGGAAAGCAAGATAACCAAGCTCATGCCGTGGTTGTGGGTGGCGTGGTTTGGTTTGGGTAACTTTGG  
(SEQ ID NO. 313)

.....:Rv270T7.seq:.....  
TCGGCTAATAATCGTCGACGCCGGCCTCCTCTGCAATCGCCTTGGCGGTGCGCGGGTTGTACCGGTGATCATCACGG  
TGCGGATGCTCATTCGGCGCATTTTCGTGAATCGTTCCTCGTATGCCACCTTGACGATGTCCTTCAGATGGACGACGC  
CGATGGCCCCGCGCGTGTGTTATCGGTCCATTCCGCAACGACTAGGGGTGTCCCCGCCGGAGCTGATGCCGTGCGAC  
AATGGCACCCACCTCCTCGGTGGGTGGGCACCGTGATCGCAACCCACTTCATCACCGCAGCCGCGGCACCTTGCGG  
ATTCGACGGATG (SEQ ID NO. 314)

#### Clone Rv271

.....:Rv271SP6.seq:.....  
CTCAAGCTTGGAGGCGTGGCGATCGCGGTCCAAGGCGCGCTCTCCGAGCACAACGAGCGAAGACNGCTCGGCGACGGA  
GCCTTTATCGACNTCCGTTCCGGCTGGCTGACGGCGGCNAAATAATGCTGGACTCGTTGTTGTCGACGGTGCCGTGGC  
GAGCCGAGCGCGCTCAGATGTACGACCGGGTGGTCTATGTGCCGCGGTTGGTGAGTTTCCACGACCTGACCATCGAAG  
ATCCGCCGATCCGCTGCTGGCGCGGATGCGCCGGTGGCTCAACTAATTCTACGGCGGCGAACTGGGTNATCCCTTCN  
CCACCGTCGG (SEQ ID NO. 315)

.....:Rv271T7.seq:.....  
CCTAGGTCACCGTACCGTCATCGGATCGGGGTGACCGCACAGATGGACTGGAGCTTCGGCGAGGTCATCGCCTATG  
CCTCGCGGGGGGTGACGCTGACCCCGGGTGACGTGTTCCGGCTCGGGCACGGTGCCACCTGCACGCTCGTGAAGCAC  
CTCAGGCCACCGGAAATCATTCGCGGCTGGCTGCACGACTGCGACGTGGTCACCTCCAGGTCGAAGGGCTGGGCGA  
GACGATGCAGACCGTCCGGACGAGCGGCACTCCTTTCCGTTGGCTCTTCGGCCGAATCCGGACGCCGAACCCGACCG  
GCGCGGGGTCAACCCGGCACCGACGCGGGTGCCGTTTACCCGCGGGGTGCACAAATCCCGACGGGTATGGGCTTTGAC  
CTGCCGACGGGGGA (SEQ ID NO. 316)

#### Clone Rv272

.....:Rv272SP6.seq:.....  
AGCTTGGCGTGACACCAACACAGGGCACTTAAGATGGCAATGCGCCGCTACCTGCACGTTTTTCGCGATGTCAGAGGA  
TGCCGAGGGGAGAACAAATGCGAGCACGGCCGCTGACGTTGCTCACCCTTTGGCGGCGGTGACATTGGTGGTGGTTGG  
GGGCTGCGAGGCCCCGAGTCTAGGCCGAAGCATATAGCGCGGCCGACCGCATTTTCGTCTCGACCGCAAGCGGACCTCA  
GCCGACGCGGTGGAGCTACTGCTGCGCGCCATCACGCCGCTAGGGCTCCGGCGGCGTCCGCGAACGTGGGTTTGG  
CGAACTGCCTACCCGGGTCCGGCAGGCAACCGAT (SEQ ID NO. 317)

.....:Rv272T7.seq:.....  
TCATGCCGTTGGACCGACCATCGGAGTTAGTTGCCGAACCGCGGGACCACCGCAAGCACCCGGTCTGGTTCGCGCACC  
GCGTCGGCCAACCGCTTGAGCACCACCACGCCGAGCCCTCGCCGCGCACGAATCCATCCGCGTTGGCGTCGAAGCTG  
TTGCATCGGCCGGTTCGGTGACAGCGCCGACCACTTGACAGCGCGATGGCGGTGAACGGTGACAAGGTGAGCTGCACC  
CCGCCGCCAATGCCACGTGCGTTTACGCGAGGCGAAGCTCTGACACGCCAAGTGAATTGCCACCAGCGACGACGAAC  
AAGCGGTATCTACGGCGATGG (SEQ ID NO. 318)

#### Clone Rv273

.....:Rv273SP6.seq:.....  
GGGTCGACTTTCTGCAAGGCGAGGCTACACCGTCGTCGTCGTTGATGCGATAGCCATCCCGTCGGGCTACTCGCCAT  
CACCGATCAGCTTCGCCCCGAAGCCGCGTGGTGATTTCCGCTGCGACCAAATGAACGGGGCCAAACCGGTATTGCT  
TACCGGCGACAACCGGGGCCACCGCGATCGGCTCGGTGTTGAGTTGGCAT (SEQ ID NO. 319)

.....:Rv273T7.seq:.....  
AATCCGAAATCCTGACCGATACTTGAACCTGGTCTCGTTCCGCAATAACTCGTCGGCGTGACAGGACGCGGCGCAAACG  
TACTTCGGCATCAACGCGTCCGACCTGAATTGGCAGCAAGCGGCGCTGCTGGCCGGCATGGTGCAATCTAACAGCACG  
CTCTTCCCGTACACCAACCCGACGGCGCGCTGGCCCCGGGCGGAACGTGGTCTCGACACCATGATCGAAAAACCTTC  
CCGGGGAGGCGGATGC (SEQ ID NO. 320)

#### Clone Rv274

.....:Rv274SP6.seq:.....  
TTCCGAATTTCCGGTCCNGGTCATATGACCTCATGGAAGAAGAAGCGGCCGCCCCGCGCCCGTGGGACGGCGAATGA  
AAACCTCACCCAGGCCGATTGAACGCCGACAAGAGGTTGGAGCAGGTGGAAGACGTCTGGACGGTCTGGGTAAGA



CCATGGCCGAGCTGAACAGCTCGCTGTACAGCTGAACAGCACCGTGGAGCGCTTGGAGGACGGTCTGGACCATCTCG  
AAGGTACCCTGCACAGCCTGGACGATCTCGCGAAACGGCTCATCGTGTGGTTCGAGCCGGTGGAGCCATCGTCGATC  
GGATCGACTACATCGTGAGCCTCGGCGAAACGGTGATGTCACCGCTGTCGGTC (SEQ ID NO. 321)

::::::::::Rv274T7.seq::::::::::  
NCTCGATCTTGGGGTACGTTTCGATGAGGCTGCTGACCAACAACCCGGCCAAGCGGGTGGGACTGGATGGATACGGATT  
GCACATCATCGAGCGCGTGCCTGCGGGTGCAGGCAACGCGGAAGAATCCGTTACCTGATGACCAAGCGTGACA  
AATTGGGGCAGCACTTGGCTGGGTGGACGATTTTCACGAATCCGTGCATCTGCCCGGAGAATTGGCGGGTGCCTTGT  
GAAGGTGGCGCCGGGGTGGCGGATCTGCCGTGCTGGATCGTCTGGTGTGCGGGTGGCGATTGTCGCCAGCAGCTGGC  
ACGGAAAGATCTGCGACGCGCTGTTGGACGGCGCCCGCAAGTGGCCGCCGGGTGTGGCCTCGATGACCGACTGTGGTT  
CGGGTGCTCCGCGCGATCGATAT (SEQ ID NO. 322)

Clone Rv275

::::::::::Rv275SP6.seq::::::::::  
TCATCCCGACCAAAACGCGAGCTAGGTGCGCATCCGGGAAGCATCGCGACACCGTGGCGCCGAGCGCGCTGCCGGCAG  
GCCGATTAGCGGGCATATTATCCCGCCGCGGCTCCCGGCTCCGAGTACGGCGCCCCGAATGGCGTCACCGGCTGGTA  
ACCGCTCTTGCGCGCCTGGGCGGCGGCTGCCGGATCAGGTGGTAGATGCCNACAAAGCCTGCGTGATCGGTATCAC  
CAACGGTGACAGCAGCCGGTTGTGCACCAAGCGCGAAGCCACCCGGTCTCCGGGTCTGTCCAACCGATCGACCGCC  
CAAGCCCACATGAACAAACCCCGGCATCACGTTGCCGATCGGCATACCGTGA (SEQ ID NO. 323)

::::::::::Rv275T7.seq::::::::::  
TTGGCGGGTTGGCCAGCAGCCCGCGGTGACGGCGACGATGCTGGGCTGGTTGCGGGCCCTGCGCCACCGCGGCTTGC  
ATGCTGGTTGGCTGTCTTGGGACGATCCCGAAATAGTCCACGCGGATCTGGTGATTTTTCGGGGTACCCGCGATTACC  
CCGCGCGGCTCGACGAGTTTGGCCTGGACTACCGCGGTGGCCAATCTGCTGAACTCGCGGCCGGTGGTGGCCTGGA  
ATGTCGAGCGCCGTTACCTACGTGACCTGATGGATCGGGGGGTGCCGACCGTGGCGGGCGATGTGTATGTGCCGGGAN  
AGCCGGTCCGGTTGCCACGCAAGGCCATGTCTTCGTGCGTCCGACCATCGGTACCGGGACACGGCGCTGTATTGCC  
GGTTTCGTGCGCGAGTTCTGTCGCGCAACTGCACGCNNGCGGGGCCAGCGGTGCTCGTTTANCCCGAGGTTCCGGTGACG  
ATGATCGTGTGGTCTCCCT (SEQ ID NO. 324)

Clone Rv276

::::::::::Rv276SP6.seq::::::::::  
GTAGGAGAGAAACAGACCGTCGATAGGACACGTGTTACGCCGTAGCTGTCTATTGGTATGGGGTGCCGCTGCCGGGG  
GGCATCTACTACCCGATCGGTTGTGGGAGGCGTTGCTGCGGGGCGACAATCTGGTCACCGAGATCCCGCCGACCGC  
TGGGACATCTACGAGTACTACGACCCCGAACC CGGCGTGGCGGACGACCGACTGCAAATGGGGCGCGTACCTCGAT  
AACGTGCGCGACTTTGATCCCGAGTTCTTCGGGATCGGGGAGAAAGAAACGATAGCGATCGATCCGCAGCACCGCTTG  
TTGCTGGAAAGCTECTGGGAAGCCATGGAACACGGCGGGCTAACACCGAACCATATGCCTCCCGACANGGGTTTTCGT  
GGGGTT (SEQ ID NO. 325)

::::::::::Rv276T7.seq::::::::::  
CGAACTGAGCCCATAGAAAGGCAGCGACTAATTCGCTGGGCAATAGGAAGACCCTTTGTCCTGCCACGTATATTTGT  
CGACCTCGTTGCGAAGGAAGCGGCTGCGATTGGTGCCCTTTCCCTGGAGAATCTCTGCCCGAGCAGGAAGTCTTAT  
GAGTTGACAAGCAGGGGCGCCGCTTCGCCGGAATCACATTCTTGGTCTCGTGAAATGAGAGCGCTCCAGGTCGCC  
GATGCTGCCGAGCGCCCGCCACGATACGACGCCATCGCGCTTGGGCGCGCTCTTCGACCACCGCCAGGTTGTGGTG  
CGTGGCGATCTTCATGATCGCGTCCATCTCGCAGGCCACCCGGCATAGTGAACGGGGACCATGGCCTCGGTTCCGCGG  
TGAA (SEQ ID NO. 326)

Clone Rv277

::::::::::Rv277SP6.seq::::::::::  
CTTAGACGCCACCTCCGGGCGAGCTCCACGGGGTGGATAAGTACGGCCGGATGTGGCCGCAATGGGAAGTTGTTGCC  
CGCTTGACTGTCCGGGTTAACGCCGATTCCACCACATCCCTTGCGAAAGGCCGTTGGGTT (SEQ ID NO. 327)

::::::::::Rv277T7.seq::::::::::  
GATCGCGATCGTTCGATGTGGCCATCCGGCTTGGCGTGCACCCGCGTAAGGCAGACCAGATGGTTCCGCGGCACGGTCAA  
CCTGCCACACGCACTGGTAAGACTGCCCGCGTGCGGTATTCGCGGTTGGTGAAAAGGCCGATGCTGCCGTTGCCGCG  
GGGGCTGATGCTGTCGGATCGACGATCTGATCGAGAGGATCAGGGCGGCTGGCTGGAATTCGATGCCGCGATCGCGAT  
ACCGGATT (SEQ ID NO. 328)

## Clone Rv278

.....Rv278SP6.seq:.....  
AGCTTACGCCGCTTTTCGCTTCNGATTGGGACGCCGCATCGAAAGCGCAGTTGGAAGCGCGGGCGCCGGCTGGTTCGAG  
CTGCTCAAGCAGCCGCAATCCAGCCCATGCCGTTGAGGAGCAAGTGGTTTCGATCTTCTGGGCACCGCGGTCAC  
CTGGACTCGGTGCCCGTCAAGGATGTCGGCGGTTCGAAACCGAATTACTGGACCACATGCGGGC (SEQ ID NO. 329)

.....Rv278T7.seq:.....  
CGACGGGACCTCGTCGCATCTTCCATAGCCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGGTATAAGGTTCGGC  
GAAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAGATGCCCTCGGGTCCNGCCAGCACTCCTCAGG  
CTTCGTGCGGGTGGTTCGCGACCGCATGGGCCACATCGCATTACCAGGTCTGCGCGAATCACCAGCACGTANACGGTT  
CCTTTCTAAGCAACACCGAAATTTAGGACCCGAATGCTCCGGGAAACATGTCACGGTAAGTCCGGTATTCCGGGT  
ACCGGTTGAGCATTGA (SEQ ID NO. 330)

## Clone Rv279

.....Rv279SP6.seq:.....  
CGGCATCGGTTTGGGCTGTACCAGCAGTTGGTAGTTCTTCACTACTGTTGTTTCGAGCGTCGAGCCGCCGCGCGTGT  
GAGGTGCGCCGACGCGTACCCGCCAGGCGGTCAGGGTGCCCTTCCAGTCCACGCNGCTGTGGTTCGGCTAACCGCTTA  
TCTTCAATCGAGACNATCGCCAGCTTCATCGTGTGGCGATCTTGTCCGAGGGCACCTCGAACCAGCGCTGCGANTAC  
AGCCACGCGATCGTGTGTCCTTCGCGTCGACCATCGTCGATACCGCAGGCACTTGCCCTTCGAGCAGCTGGGCCGAT  
CCGTTGGCAACGACCTCAGAGGCACGATTGGACATCAGCCCTAGCCGCGCTGCG (SEQ ID NO. 331)

.....Rv279T7.seq:.....  
CCGTGCGANGCCCGACTTGGCTTGACCGACACCAACATGGCCTGAGGGTGTTCACAAGACCGTGGCCGACGGGGCTG  
AACATCACCATGAGCGGCATGAGCCACGCCACCGAGTTCATCATGTTGATCGCCGAAAACATTGGCGGGTAGCGGAA  
GAACGGTCGAGGTGCTCTACACCGAGTATTCGAAGTCGAAAGGCCAACCGCTGCTCAACGGCGTCAACATCATTTTCG  
ACGGGTTTCTGCGAGGGAGGATGCCACGATGAAGTGGATCCAGGTGCTGTTGATCGCGTCGATCATCGGGTTGCTGTT  
CTACCTGTTGCGGTGCGGCCGAAGCGCGCGGTCCGTGCTGGGTCAAGGTGGGGTATGTCTTGTTCGTGCTCCCGGCA  
TCTATGCCGTGCTGAGA (SEQ ID NO. 332)

## Clone Rv27

.....Rv27SP6.seq:.....  
TTACACGNCCTGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGAC  
CATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTTTTCGAGCGTCGCGCGGGGCAGCTTCGCCGG  
CAATTCTACTAGCGAGAAGTCTGGCCCGATNCGGATCTGACCGAAGTCGCTGCGGTGCGAGCCACCCTCATTGGCGAT  
GGCGCCGACNATGGCGCCTGGACCGATCTTGCCGCTTGCCGACGNGACGCGGTANGTGGTCAAGTCCGGTCTACN  
CTTGGGCCCTTTGCGGACGGTCCCGACGCTGGTTCGCGGTTGCGCCGCGGAAAGCGGCGGGTTCGGGTGCCATCAGGAATG  
CCTCACCGCCGCGGCACTGNACGGCCAGTGCCGCGGCGATGTCNGCCATCGGGACATCATGCTCGCGTTCATACTCCT  
CGACC (SEQ ID NO. 333)

.....Rv27T7.seq:.....  
CAGGCATGCAAGCTTTGTACACCAAGTGTTCGACCAGGCGCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCA  
GGTCGCCACACGCTGGTCAGTGCCTTCAGCTCGCTTGCGGCGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTG  
GCGCAGCTTGGGGATCGCGACGTCGATGTTGCGGCACGGGTGTCGAAATCACGGTGGCGGTAGCCGTTGCGCTGATT  
GGACCGCTCATCGCTGCGTTCGCGGTAGCCCGCCCCGCACAGGGCGTCGGCTTCAGCCCCCATCAAGGCGG  
(SEQ ID NO. 334)

## Clone Rv280

.....Rv280SP6.seq:.....  
AGCTTAGCCAGTTTTTCTACTCTTGGGCCACACCCACAGTGCTTCGACGGTACGGTCACCCATGATGGCCATCCAGT  
TGGCATCGGTGAGCTGATAAATGCCAGCTGGTTTCGCCAACCCGGTAGCGATCTTGGCGCGCTGCTTGTGTCACTGA  
TACCTATCGAGCAAGACAGCCCGTTTGCAGACAAGATGACTTTTCGGATCTCTTCGGCGACTTCGATGGGGTCGTTCGG  
GAGTCCCGGGGCGCCACCGCGAGGTAAGCCTCGTCCCAGCCCCATACCTCGACCGGGTATCCAGGTGCGCGCAATAACG  
CCACCACCTCCTCGGACGCCGCGTTGTAGGCGGCTGGGTTCGACGGCAAGAAGTGGCCTCAGGGCATCGTCGGCGCGG  
TCCCAACGGCNTGCCGGCGCGCACACCGTAGGCGCGGGGCTC (SEQ ID NO. 335)

.....Rv280T7.seq:.....  
CCGGCGGAACTCAGACGTGCTGGTGGTTCGGCATGGCACCGCGGGCAGCAAAGCGCACTTCTCCGGGGACGACAGCAA  
GCGACCGCTAGACAAGAGGGGTCTGCGCAGGCAGAAAGCGTTGGTACCACAGCTGCTGGCGTTCGGCGCCACCGATGT  
TTATGCCGCGGACCGGGTGCCTGCCACAGACGATGGAGCACTCGCCGCGGAACTGAACGTGACCATACACAACGA  
GCCACCCGTGACCGAAGAGTCTACGCCAACAACCCAAACGCGCGCCGACACCGAGTGCTGCAGATCGTCGAGCAAGT

AGGCACACCCGTGATCTGCACGCAGGGCAAGGTCAATCCCGATCTGATCAGTGGTGGTGCGAGCGCGACCGTGTGCC  
CCCGACAGTCCCGCAATCGCAAAGGCAGCACGTTGGTGT (SEQ ID NO. 336)

Clone Rv281

.....Rv281SP6.seq:.....  
GTATGGTCAGCTGTCCATCCGGCGCTGTCGGCCGAGCTGCCAGATCTCGTCAGCCGTAACCGGGTTGCGGGATCCACG  
CGTGCGGGTTGTCTAC (SEQ ID NO. 337)

.....Rv281T7.seq:.....  
CCGACTTTCCGCGGGTACCCGCTCAACTTTGTGTGNACCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCA  
ACTTCATCCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACT  
ACATCATTGCGACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCACTGGCGAAC  
TGGTTCAACCAACTTGAAGGTGATTGTTAACCTGGGCTACGCGACCCGGCCTATGGTTATTGACCTCGCCGCCCAA  
TGTTGCGACTCCGTTGCGTTGTTCCAGAANGTCAGCCCG (SEQ ID NO. 338)

Clone Rv282

.....Rv282SP6.seq:.....  
GCACCGATGTCGGCGAGCACTTCGTCAACTTCCAGGGGTGCCCGCACCAAGTATTTGACGAGTATTTCCGTGCGGGC  
GCCGCGCGCGGTGCGCGGCAGGTGGTCATCCTGGCGCGGGGCTGGGACTCGCGCGCGTACCGGCTGCCTCGGC  
(SEQ ID NO. 339)

.....Rv282T7.seq:.....  
TGCACCAACTTACTGAGCATGCTAACGCTGGTCGTGCGGGTCTTGTTCGCCGCTGTCGGGCAGGGCACACGCTCGGGG  
CGTAGCTGGGAGAGGCCCGGTCAGCCCGGAGAGCAGTGCTCAGTCCGCCAGCTTGACCGACTTTCGATGAGAACGC  
GCTTCTCGCCGATTGAAGTGGCGTGCTGACGGTCGCTGAGCAGCGCTCGCCGAGTGCGGCCGCTGATTCTTTCATCG  
AGCCAGGACGCGCATTCTGTGTTGCGCCGC (SEQ ID NO. 340)

Clone Rv283

.....Rv283SP6.seq:.....  
AGCTTACGGCCGGTCGACGCGACGAGTGGTTCATGACACCACAAACCGTCAACGCCTACTACAACCCGGGGATGAACG  
AAATCGTCTTCCCGCAGCGATTTTACAGCCACCATTTTTCGATCCGCGAGGCCGACGAGGCCCAACTACGGCGGGAT  
CGGGGCGCGTGATCGGGCAGCATGATCGGGCAGGTTTCGACGATAGGGCGCCAAATACGANGGCGACGCAATCTGGT  
CNATTGGTGGATCGA (SEQ ID NO. 341)

.....Rv283T7.seq:.....  
ATGTCGTCACTGTCACCAATCGCGAGGACCCAATCATGCCGCCAGGGCGGCCAACCCAATGGTGGCCGCGAAGCGG  
CAGCTCGATCGCAGCGCGGAGGTGCCGGCCGCGAGTTGATTACGAACAGGGTGAGGTCATAGGCGGGCAGGATAGTG  
ACGAACGCAAGACCTATATCTGCCGTCGGAGTAAGAATCGAGTAGCCGGTCGACCAACGGAAGCGAAAGTGTCCGCGA  
TGTTGATGAGCGTCGCCGTTGTGGCGCGGTGGC (SEQ ID NO. 342)

Clone Rv284

.....Rv284SP6.seq:.....  
AGCTTACAGCGTGGCGATGCTGTTGCGNACACCTCCCTACTATGCGCAATTCGCCGACACGGGTGGCATCAACACG  
GGCGATAAGGTGGACATCGCTGGGGTGAACGTCGGGCTGGTGCGCTCGCTGGCAATCCGCGGCAACCGCGTGTGATC  
GGATTCTCGTTGCCCGGCAAGACAATCGGGATGCAAAGCCGGGCAGCAATTCGCACCGACACCATCTTGGCCGTAAG  
AACCTGGAAATCGAACCCCGCGTTTCGGAGCCGTTGAAACCCAACGGTTTCTGCGGTTGGCGCAGAACACTACGCCA  
TACCAATCTATGACGCGTTCGTC (SEQ ID NO. 343)

.....Rv284T7.seq:.....  
CTGCCGCGGTGGCGGTGACGCGCTGGCAAGTCAACCGCACCGCGTCCGGTTCATCGGCAGGCTCCCCGAAAAGGGCC  
CTGGCAACAGAGGTGATCAATGAGCTCCCGCAGACCTTCGCCGATCTGGGACCGACATACGTGAAGTTCGGCCAGAT  
CATCGCGTCCAGCCCGGGAGCATTCGGTGAGTGCCTGTGCGGGGAATTCCGCGGCCTGCTCGACCGGGTGCCGCCCG  
CAAAAACGACGAGGTGCACAAGCTCTTCGTGAGGAACCTCGGCGACGAGCCGGCCCGGCTGTTGCGCTCCTTCGAGG  
AAGAACCCTTCGCGTCTGCGTCCATCGCCCAAGTGCACTACGCGACCTGCGCAGCGGCGAAGAAGTGTGGTCAAGATC  
CAGGCCCGGGCATCCGCCCGCGGTTT (SEQ ID NO. 344)

Clone Rv285

.....Rv285SP6.seq:.....

GATCGTGCCGGCCCCCGGCGGCAGTAGCAGATCAGCTCGTGAATCGCGGCAACCAGTCCAGTCGATTTCATACG  
GGCGCCGTCAATCAACTCTGCGAACATCGCGATCGGCACCGGAAACCGGCGAGCCGCTCAGCCAGCGCAACCAGCAC  
CGGGATCGGATGAATCATCAATATTATCAAGTGATTTCTGATGGCATCGAGCTCGGTGATCTTGGTCTCGGGGGCCA  
GCTCGCCGTGCGCGACGTCGTGATCCGGCGGCGGAGCGCATAGACCGCAAATAGTCCGCTCGCTTTTCGCGCGGCA  
AGAGTCGGATGCCGTAATATANGTTTCTGGCGGCCGTGCGCGTGATCNACTCGGTGATTTCGATACGCCCTGTTTCATCTC  
GGTCATGCCGTCTC (SEQ ID NO. 345)

::::::::::Rv285T7.seq::::::::::  
GGTGGCGCAATGACCGAAACACCCAGCCCCGCAAACCCCGGCGCCCCGGCCGGGGCCGCACAATCGTTCGTGTTG  
GAGCGGCCCATCCAGACCGTTGGGCGCCGTAAGGAGGCGGTGTTACGAGTGCGGCTGGTGCCCGGCACCGGCAAGTTC  
GACCTCAACGGCCGAGCTTGGAGGACTACTTCCCAAACAAGGTGCACCAGCAGTTGATCAAGGCACCCCTGGTCACC  
GTGGATCGGGTGAAAGTTTCGACATCTTGGCCACCTGGGCGGCGGCGGCCGTCGGGTGATGGCCGGCGCGCTGCG  
CCTGGGTATCGCCCGGCGATTGATTCTNGTATCGCCGGATGACCGGCCGCGCTGAATAANGCCGGCTTCTTGACCGT  
GATCCACGCGCCACCGAACGCAA (SEQ ID NO. 346)

#### Clone Rv286

::::::::::Rv286SP6.seq::::::::::  
CACAAATAGATTACTCAAGCTTCGAACAGCGGCCTTATCAGTATCCCCGCTGAGACCTTGACCCTTAGGGCCGAAGT  
GACTTCGCTGCTGCTATGCCGACACCCGATTTCAGACGCTGCTGTTACACGACGGCCGGGCGGTGGCCACCATCAC  
GCTCAACCGCCCGGAACAGCTCAACACCATCGTCCCGCCCATGCCGACGAGATCGAGGCGGCTATCGGGTTGGCCGA  
GCGCGACCAAGCATCAAGGTCATCGTGCTGCGCGGTGCCGGCCGCGCCTTCTCCGGCGGTTACAACCTCGGCGGCGG  
GTTCCAACATTGGGGGCGAT (SEQ ID NO. 347)

::::::::::Rv286T7.seq::::::::::  
TCAGGACGCTTATGGTTGGCAGATGGTCGCCCTGGCGTCGAATACGCGCGAGCGCATGAGCTCACCGGTTCCGAACAA  
CGTATCGAAGACGTGCGACTGCTGGCAGATGGTATCTCCGATGTGGTTGTAATTTGTATCCCAACTCTAACTGTGCT  
ATCGGATCAGCGTGAATATCGAGATATTGCGAATGCGATGACAGGCGGCCATTTCGGTTTATTTCGCTTACGCTTCCCGG  
GTTTCGATTGCTGATGCACTGCCGAAACGCGGATATGATTGTTGAAACCGTATCTAACGCAATTATTGATGTGGT  
AGGCGGCAGCTGCCGTTTTGTGCTGTGCGGCTATTTCATCGGGTGGGGGTGTTTGCTATGCCCTCTGCTCCCAT  
(SEQ ID NO. 348)

#### Clone Rv287

::::::::::Rv287SP6.seq::::::::::  
CGCAGCTGTCGCGGATCTGGTCCGGAATACCTAGCTCCAGGTTCTGAGTGGAGATGAGTGCGGCCATCGAAGTGTGT  
CAATGTACTCCAGGATGTGAGGTGCCAGGCGCTGGCGAGGATCTTGGGCACCGCCGCCATGACTTGGTTCGAAGTCGG  
CGAACGGGGCGAGCAGCTGGCGTCTGCTG (SEQ ID NO. 349)

::::::::::Rv287T7.seq::::::::::  
GTAGTTCGTTTCATCCAAACACAGTGCGGTACCGGCTCAAGCGGATCACCGACTTCACCGGGCGCGATCCCACCCAGCC  
ACGCGATGCCATGCTCCTTCGGGTGGCGGCCACCGTGGGTCAACTCAACTATCCGACGCCGCACTGAAGCATCGACAG  
CAATGCCGTGTCATAGATTCCCTCGCCGTCAGAGGGGGTCCAGCAGGGGGCCCCGGAAGATACCAGGGGCGCCGTC  
GGACCGA (SEQ ID NO. 350)

#### Clone Rv288

::::::::::Rv288SP6.seq::::::::::  
TCCGCTCGCTTCTCCGAGAGGTTGAGTGCCAACGCTCTGCCGATGCCCGAAGCCGGCCCCGGTGATGACGGCGACCTT  
GCCTTCGAATGAGCTCATTTGACTACTCCCCGTGGTTGTCCCTGCGATTGGTGGAGGTGGCCGCGCAGCCTTGCCCCG  
AGGTGCGCGATCGCGTCTCGGGCTTCGGGGAGCAGACTGACCTGCAGATGGAAGTCGTGCCACATGCCCGCGAACCCG  
CGATGCTCGATGCTTGTTCGAAGCGGCGCAGGCGGTTTCGATCTTGTCCGCGTCAACACNGATCGGATCGTCGCC  
CGGCTGTCATGACGAATGGGCG (SEQ ID NO. 351)

::::::::::Rv288T7.seq::::::::::  
ATGGGAGGCCACCGATTACCATCTTGACACACCCGATTCCGGGCTATTGATGTCCACGTTCCGGTCCGCGAACCGCGCT  
GTGGCTGCTGCTGGCCAAAGGCGGAGGCGATACCGAAGTCAGTGCCCAAGCTTGGGTTCCACGCTCGCGCAGCCACGC  
CGTCACCTTTCCACGAGACCTCACCTGCCGATCCGAAATGGAATCGGCCGTGACGGAATTGGCGCAGCGAACACTCAA  
CGAGTGGTGGCTTCGTGCGGAACCGTCACCCGAGTCGCGGTACCGTGCGCACGGCGACGTTCTACACCCGCACCAA  
GATCCGAAAGCTGCAAGCTCCACGACCGATCCCGACGTCATCACCGCTGCCGCCCGGACGTTCTTGAACCTATTCG  
AGCTGGAATCGGCCGTCCGGTTGCTGGGAATTGCNGTTAAGAACTGGGCT (SEQ ID NO. 352)

## Clone Rv289

.....Rv289SP6.seq:.....  
GCTTTGCGCGCTTCTCCGAGAGGTTGGAGTGCCAACGCTCTGCCGATGCCGAGCCGGCCCCGGTGATGACGGCGACC  
TTGCCTTCGAATGAGCTCATTTGACTACTCCCCGTGGTTGTCCCTGCGATTGGTGGAGGTGGCCGCGCAGCCTTGCCC  
CGAGGTCGGCGATCGCGTCGCGGGCTTCGGGGAGCAAACCTGACCTGCAGATGGAAGTCGTGCCACATGCCCGCGAACC  
GGCGATGCTCGATGCTTGTTCGAAGCGGGCGCAGGCGGTTGATCTTGTCCGCGTCAACGCAGATCGGATCGTCGCC  
CGCGGGTCTGCATGAAGAAT (SEQ ID NO. 353)

## .....Rv289T7.seq:.....

CTCACGCAGCCACGCCGTACCTTTCCACGAAGACCTCACCTGCCGATCCGAAATGGAATCGGCCGTGACGGAAATTG  
GCGCAGCGAAACACTCAACGAGGTGGTGGCTTCGTGCGGAACCGTCACCCGAGTCGCGGTACCCGTGCGCACGGCGAC  
GTTCTACACCCGACCAACATCCGAAAGCTGCAAGCTCCAGCACCGATCCCGACGTCATCACCCTGCCGCCCGGCA  
CGTTCTTGACCTATTCGAGCTGGATCGGCCCCGTCCGGTTGCTGGGAGTGCGGTTAGAACTGGCCTAGAAACCGGCGG  
GCACACCGCACCTGGGCGGGN (SEQ ID NO. 354)

## Clone Rv28

.....Rv28SP6.seq:.....

TGCTTCCGGCTCGTATGTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG  
CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACC  
ACNCGCGGGTCGGGCGCGGGTCGCCANGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCCCGGC  
TGCGCTACGTCGAGCCATACCGGGCGGAGCTACATCGGCTCGGCCGCCAGTGTTCGGGCCCTCTTTCGAAGTCGAAG  
TCGATACCGATTGCGCATCCGCGGCCGCA (SEQ ID NO. 355)

## .....Rv28T7.seq:.....

CAGGCATGCAAGCTTCACGTCCGTACGGCTCGGGTACGCTTCGGTCGCAGTGTGCGAGTGATAGATGACGACCGGGAC  
CTCGTCTGCATCTTCCATAGCCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGGTAGAAGGTGCGCGAGCGCTC  
GGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAGAACCCTCGGGTCCGGCCAGCACTCCGCAGGCTTCGTGCGG  
GTGGTCGCGACGCGCATGGGCCACC (SEQ ID NO. 356)

## Clone Rv290

.....Rv290SP6.seq:.....

GCTTGTCTATCGTCCCGGCCAGGTCCGGCCAGTCAAGGTGGAAGGCCAGTCCGGTCTCTCTCCGACTACGGCCAAGA  
ACTGGGCGACGGTGTCAAGTGACAGACGCGGAACTGGTGCGGCCCTAGGCGAGCGACCGCTCACAAACGGCGGTGA  
CCGCGTTCTGGTCGTGCACCATCGAGCCGTGCCAGCCCGGCCGCGTCCGTCAGCCGCATCCACTGGATGCCCTTCT  
CGGCGGTTTCAATCAGGTACAGGCGACGTTGCCACCATCGTGCCGGGGCACGGTTAGCGAGAAACCGCCGACTTCAC  
GATTGCCTCGGTGATGCCGTGAAACAGATCGGGCCT (SEQ ID NO. 357)

## .....Rv290T7.seq:.....

GCGCGCCATGTTGAGGTTGTCCGACGGTGACGACGGTGAACCACAACCTGTTGACCTGTCCGCACACACCGTGTGGAT  
CGGCGAGCGGACCCGACAAATCGATGGCGCGCACATCGCGTTTGCCAGGTGATTGCTAATCCGGTCCGGGTCAAGTT  
GGGCCCCAACATGACCCCGGAACTGGCCGTGGAGTACGTGAGCGGGTCGACCCGCAATAAGCCGGGCGGGTAC  
TTGGTGAGCAGGATGGGCAACCACAAGGTCCGCGATCTGTTGCCACCGATCGTGAGAACGTCCATGCCACCGGGCAT  
CAGGTCATCTGGC (SEQ ID NO. 358)

## Clone Rv291

.....Rv291SP6.seq:.....

TTGCCTTCCATGCCGAGCAAGGTGCACTCAGCGATGACGAATTGTTCTTCTTCGCGGGTGTTGCTGCTGGTTGCGGGC  
TATGAGAGCACTGCTCATATGATTAGCACATTGTTTCTGACGCTGGCCGACTATCCAGATCAGCTGACACTCCTTGCG  
CAGCAACCAGACCTGATCCCGCCGGGATCGAGGA (SEQ ID NO. 359)

## .....Rv291T7.seq:.....

CGACGCTGGGCCCAACTGCGACCACAGGTCTGGTATGGCAGGACATGGCCGGGTTACGCGGCGCCAATACCG  
(SEQ ID NO. 360)

## Clone Rv292

.....Rv292SP6.seq:.....

TAACGACTCGGGTCCAGCGACCGCGCAACACNAACGGCCGGACNACGTGGGCCAGGGTCGCGGCCCTCCCCTACAAAC  
AGGATCCGTTGCCTGCGAACGACAGGCTCCGGTGCGGCGTTGGGCGCCGTGCTCGTCCAGCGTCCGGTCCCGGGTCG

CCGGCGACGCTTGTTCCTCCATACTCGCCCCCTAATCTCGAGGCAGCCCGTACCCGCAGGCAACCTCCCCAAAATGC  
AATCCCCCAAAATGCAATGCGTCNAGCTATTTCTCACACCGACCGCTAGTTGCGGATCANAAATCCGTTGGGCGCGGA  
(SEQ ID NO. 361)

.....Rv292T7.seq.....  
CNTGGCGGTGGGTGCGGTGTCGAACACGACCACACTTCTTTGCGGTTCGGTGATCTCGACACCGGCCGCGAGCCGACC  
ACCATGCGCGCGTAGATCGGCGATCAGCGCGTCTGGCTATCGCCTGGGTGCCGCCACCGGAATCGGCCAGCCGACCGA  
ATGGGCCAGCGTTGCCATCATCAGTCCGGCGCCGGCCGACACCAAGTGACGGCAACGGTGAAATCNCGTGGGCGGCAAC  
GCCGGTGAAACAACGCGCGGGCATCTCGCCCGCCAGCGACCGCCAGGCAGGGGTGCCCTGGGCCAGCATCCGACGCC  
GAGACNCAGGACCGANCCAGTG (SEQ ID NO. 362)

## Clone Rv293

.....Rv293SP6.seq.....  
GCTTTTCNGATCGCAGCGAGTCGTACCCGCGCCGGTCACTTCGTGGATATCGCCGGCCTGGTCAAGGGGGCGTCCGA  
GGGAGCCGGGCTGGGTAACAAGTTCTGGCTCATATCCGCGAATGCNACGCCATTTGTGAGGTGGTGCGGGTGTTCGT  
CAACAACNACTTGACTCATGTACCGGACGGGTCTGATCCCCANTCCGACATTGAGGTCTGCGANACCGAGCTGATCCT  
GGCANATCTGCAAAACCCTGGAGCGGGCCACGGGCCGGCTGGAGAAGGAANCGCGCACCAACAAGGCGCGCAAGCCGGT  
CTACGACGCGGCACTGCGTGCCAGCAGGTGCTCGACGCCGGCAANACGCTGTTCCGCCGGGGGTGGATGCCG  
(SEQ ID NO. 363)

.....Rv293T7.seq.....  
GTCGTACGCCATTNGTCGGTGTGCGCATACCAAGTACGACGCGCCGGGCACCTGACGCGGGCGGCCGCGACCAAGTCCGGT  
GCCATCGCCATCGTCTGCCACCCGGTCAACGGACGCACCTTCTCCTGGCCGACGTAGTGCGCCACCCGCCGCCGTTG  
CGTCCCATCNATCCGGTCAACATGAGCAGCGCCAACACCGAGCGGTACATGACATCGCTGTGGAACCAAGTACAGATT  
CCGCCGCCCATGATGATCATCGACCGTCTCCGGATTTCGGTTCGCGTTCGCGGGCGAAATTCCTTGGCAAACCGGATTGC  
CTGCGCGGCCGGCACACCGGTGATCGACTCCTGCCAGGCCGGGTGTTCTGCTGGGTTCGGTCTGGTACCGGT  
(SEQ ID NO. 364)

## Clone Rv294

.....Rv294SP6.seq.....  
GCGAGGCGGTATCGCTTCCCGTCGTACCGGCGACCGCCAGCCGAGAAGCTCGTTTTCCAGTGTTGCTGGGGATTCTC  
ACGCTGCTGCTGANTGCGTGCCANACCGCTTCCGCTTCGGGTACAACGAGCCGCGGGGTACGATCGTGCGACGCTG  
AANTTGGTGTTCTCCATGGACTTGGGGATGTGCCTGAACCGGTTACCTACNACTCCAAGCTGGCGCCGCTCTCGTCCG  
CAGGTGCTTGCTTGCATAGCCGGGAGGCCGGATCCGCAATGACGGATTCCATGCCAACGCTCCGAGTTGCATGCGG  
ATCGAATACNAATTGATCACCCA (SEQ ID NO. 365)

.....Rv294T7.seq.....  
TGGGTCTTGCCGGCGAGCCAGCGAAGTCGCTAGCGTGGCCGTGTTTCTTGGCTTCGGATCTATCCTCGTTACATGAC  
CGGCACCGTGTTGGACGTGACTGGCGGCCGGTTCATATGACACCGAGATCATTGCCACGGTACGGCAATTCTGTCAAGA  
AGGAAATCTTTCCNATGCACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGAAATCGTCGATCGGCTGGGTGTTA  
TTGGCTTGCTCGGTGCGCGGCTGCAAGGTATCGACACCACCGAGTTTATTCTCGGGCGTGCCGGCGCATTCGAGCTG  
GCGGTGCGCGCTGCCAGCACCGTCTAAGTACTTGANGATGGTCAAACGTTCGGACGAACCGCCACCACGTGCTGCC  
GAACGG (SEQ ID NO. 366)

## Clone Rv295

.....Rv295SP6.seq.....  
TAGATGCCCAAGCTTGCCNTTANAGACCTCGTCGACCAAGCACGGACCGTCTGAAGGTGGCGAATCCGGGGCTTG  
GCGTCNACCCGCGTAAGGCAGACCAGATGGTTTCGCGGCACGGTCAACCTGCCACACGGCACTGGTAAGACTGCCCGCG  
TCGCGGTATTTCGCGGTTGGTGAAAAGGCCGATGCTGCCGTTGCCGCGGGGGCGGATGTTGTGGGAGTGACGATCTGA  
TCGAGAGGATTACGGGCGGCTGGCTGGA (SEQ ID NO. 367)

.....Rv295T7.seq.....  
TCTCCACGGCGTGGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTCTGCGTTAG  
CGCCGGATTCCACCACATCCCCTTGCGAAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCCATCGAGATAGTGG  
AGCAACGCAATCCGTGCGGTACGGTTCCGGTCTGACTCGATGTCGCGACCTTGGCGTTGACACCATCTTTGTCATTG  
CGCGCAAAGTCGATCATCCGGTAAGCGCGCTTATGACCGCCGCTTTGTGCCGGGTNGGTAATCCGGCC  
(SEQ ID NO. 368)

## Clone Rv296

.....Rv296SP6.seq:.....  
GCCCGGTTTCGATCGGGCATGTCCGCAGTCGTCTACCGGAGGCGGTCGTGGCCGCGCTAATCGGGCGTCGGCGCCGAC  
AAGATGTGGGATATCCGCAATCGGGGCGTCATCCCTGCGGGCGCGCTCCCCCGCTCCGAGCCTTCGTGACGCAATC  
GAGGCAAGTCACGACGCGGATGAGGGGCGAGCAGTGAATTACAGCGAGGTCGAGCTGTTGAGTCGCGCTCATCAACTGT  
TCGCCGGAACAGTCGGCGACCGGGTTGGATGCGGGCACCACACCCTACGGGGGATCTGCTGTCTCGGGCTGCCGAC  
CTGAATGTNGGTGCGGGCANCGCCGGTATCNACTCCCGTGAACACAGCCGGGC (SEQ ID NO. 369)

.....Rv296T7.seq:.....  
CTCGGCGTGGATATCGGTGTAGCCGGCGCCGGTGAANGTCGGCTCCTTACGTCCACTCGACAACAGCTCATAGCGATC  
CAACCAAGTANGCAACCGCCTTCAGCAGTACAACCGCGCCGCGAACACTGCGAGTTGAACGCGAGCTGCCTGGGTCAG  
CATGCCTCTGCCGTTGTTCAGCCGAAGGCCGCCGAACAGGTAATGCGTCAACAGGCTCGCTAGAAACGCCAGAACCAC  
GGCCACGAACAGCCAGTTTCAGCACCGACCGGTAGAACGGCAGATCGAAGACGAAAAAACCAATGTCATAGCCGAATT  
CGGGGTCCACGATGCCAAAGGTGCCCCCGTGTACAACAACCTGAACCTTCACCCA (SEQ ID NO. 370)

## Clone Rv29

.....Rv29SP6.seq:.....  
TCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAA  
GCTATTTAGGTGACACTATAGAATACTCAAGCTTCACGTCGGTACGGCTCGGGTACGCTTCGGTCGCGAGTGTGCGAGT  
GATAGATGACGACCGGGACCTCGTCGGCATCTTCCATAGCCGCCACACCTTCAGTTGCTCACCAGGAATCCAACCGGT  
AGAAGGTGCGCGAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAGAGCCCTCGGGTCCGGCCAGCA  
CTCCGCGAGGCTTCGTGCGGGTGGTCGCGACGCGCATGGGCCACCATCGCATTACACAGGTCTGCGCGAATCACCAGCA  
CGTAGACGGTTCCTTTCCTAAGCAACACCGAAGTTTCAGGACCGAATGCTCCGGGAAACATGTCA (SEQ ID NO. 371)

.....Rv29T7.seq:.....  
CAGGCATGCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACCACGCCCGGGTTCGGGCGCCGGGCC  
CGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCAGCCACCGCGACACCACCGGCTGCGCTACGTCGAGCCATACCGG  
GCGGAGCTCCATCCGCTCGGCCGCCAGTGTCCGGGCCCTC (SEQ ID NO. 372)

## Clone Rv2

.....Rv2SP6.seq:.....  
CCTGCATCCGGCTCGTATGTTGTGTGGAATTGTGANCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTA  
CGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCCAATCCCCCTGCCCTGATACGCGTCGGCAACCGTGAA  
CGCGATCTCGGCGACCGTCGGATCGGTTTCATCCCGCAGAAACGCGCGTCGGCTACGGGGTTCGCTTCCGTCGGTCAC  
CAGCCAGACGAAGTGGTCGACGTAGTCGACTTCCGACAGGTAGTGCATCAACGCCGGACTGGGAACACNAGCCGACAT  
GAACCGTCGATACAGCGTCTCNCCGGAGAACTGGATGTGTCCGTGCACGGTCCGCTCGCGGTACCCGGGCGAGCACGGG  
GCGTAACATCAGTTGAGTCCCGTCGGCAAGCGGTACCGGAATCGGGGAGACGA (SEQ ID NO. 373)

.....Rv2T7.seq:.....  
CAAGATGATCGCCGGTGCCACCCCGATCCGTGCCCTCGGTGAGCGCGAACGTGCTTTCCGGTCCGGCGACCAACATGTC  
GCACGCACCGACAGGCGCAACCCGCCGGCCGCCACATGCCCCGTTGATGGCGCCGACCAACCGGCGAGCGGCGACTCGAC  
GATGGCGCGCAACAGCGCCGTCATTTCCCGCGCCCGCGCCACGCCCATCCGGTACGGATCACCACCACCAACCGCCGGC  
CTCGCTGAGGTCCGCGCCGGCGCAGAACGTTCCGCCGGTATGCCCCAGCAGCAGCAGCCGCGACCGCCGGATCTGCTTC  
GGCCGCACTCAGCCCTTGATGTAGTTGGCTGACCAGCGTGCTCGACAGCGCGTTGCGGTTGTGCGGAGAGTTCAGTGT  
CAGCCTGGCGAAGGGGCCGCCGAGGCGGCCGGCCAGCGTAGTCGACGGGGCTG (SEQ ID NO. 374)

## Clone Rv301

.....Rv301SP6.seq:.....  
CTCAAGCTTCGATCGACAGTACTCCCGCCTTGGGTCTGGTCTTCGAGCTGGTCGGTCATGGTCGGACCTGCTGGTAGT  
GGGGATCTAACGCAACATGGTCGGGATTCATCATGGTGTACCCGTGATACCCATTTCGAGCTGCCGGTGAAACCCCGC  
GATGCCGGGATTTCCAGCCGCACTAGGATGTCTAGCCGGCCAGCCGCTGCCGCCGGACTTCGGGATGTTCCGGTATACC  
ACCGATCGGCAATCTTGCNTATCCGCCGATGCTCGAACGCTAGCCACCCCAAACCAACCACTGTGACNACAATC  
(SEQ ID NO. 375)

.....Rv301T7.seq:.....  
TGAATTTCCCGATCCCAACATCTCGGTTTCAGATACAGGTCGCCATACCCCTTACTTCGGCAACGCTGGGCGGATTTGGC  
CCTGCCGCTGCAGCAGACCATCGACGCCATCGAATTCGCCGGCAATCTCGTTACGCCAATCCATACCCATCGACATTCC  
GCCGATCGACATCCCGGCCTCCACTATCAACGGAATTTTCGATGTGCGAGGTCGTGCCGATCGATGTGTCCGTCGACAT  
TCCGG (SEQ ID NO. 376)

## Clone Rv302

.....Rv302SP6.seq:.....  
TACTCAAGCTTGAACGCTGCGAGCGAGCCCATGTAGAGCGTTTGGTACCAAACCGATCGGTGGGCGCAACTTGCCATGG  
GCTCACAGCGGCTATCGCGAGCGGTGTAGCCGATCATCGGCCAGGCGACGGTGGCCTGAGCGGCAGGGGTTGCCTTATC  
CATCCTCTTGGCGCATGGTTGCCGAGGGAGTGCCGGTAAGTCTGGTGGCAACCTGGCCCGCTGCGGGTTGGGTTTCG  
GATTCCCTCGGCTAGTAAGGTGCTCGCCTGGTGTACAAACGAATCGCTAGACAGCTCTTATCGGGAGTGCCCGTCGCG  
ATCGTTGCGCTGCCGCTGGCGATCGCGTTCGGCNTTACCGCCACCGGAACGTCCCAAGGTGCGCTCATCGGGCTCTAC  
GGCGCCATCTTCGCCGATTCTTCCNGCCGTGTTCCGTGG (SEQ ID NO. 377)

.....Rv302T7.seq:.....  
GCGGTGTCTGAACCTTCGCCGTTCCCTCCAGCGCATTGAGCTTCAGCCCGACCGGCAGGTAGGGAGTCGGCATGCGGT  
CCTTCGCCCCGACCCCGCTGGCTAAATAGCCACCCCGAGCGCGGTACCGGTCTTTGCACCGGGACGACGGCATACCG  
GCAGCGGCAACATCGCCGCGGGCTGCAGCGTGAACGTGCAATACGAGTCGAACAGTGTGCGGCGGTAAAAACCCGAGC  
CGGCGGTTCGTTTCGGTAATCAACGGCTCCTGCGCAACACAGCTGCAANTCNCCGGTGCCACCGGCGTTGACAATCTTGA  
TNTCGGCGACCTCGCGCACCAN (SEQ ID NO. 378)

## Clone Rv303

.....Rv303SP6.seq:.....  
TACTCAGCTTCGGCTCAGGTGGTGTGCTGTTAAAGTTCNCTGAACGGTGCAGGTTTCGACAATGTGGTGCCGGTTTCG  
GCGGGTACTGCCATCGAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTACAAACAAATCGCGGTATGCGTTCTT  
GAGCATGAGTCGGCGACCGTCTCATGGTGCACACCCACGACGGAAGACGCAGATCGCCGTCAAGCNTGTGTGCCCG  
GGATTATCAGGACTGACCTCCTGGCTGACCGGCNTGTTTGGTCNCGATGCCGCGCCCGCGCGCGT (SEQ ID NO. 379)

.....Rv303T7.seq:.....  
CATCACTGGTTTCATGAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCGGCGG  
TCGGGTGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCTGAAACAGCTTCCATATCCCGCGACGAACG  
ACGCCAGTCCGCTACGTAAACCTCCGCGACTGTCCATGGACAACANCGGTTCTCCACCGACCGGGCCCGGTGTGG  
GGTGT (SEQ ID NO. 380)

## Clone Rv304

.....Rv304SP6.seq:.....  
CTCAAGCTTCCCGGCGGCCAGTACCGAAAGCGCGAACAGCTCGCGGCGAGCCCAACNTGCTGCGTCGGATTGCCGGC  
GGCGANATCAATTCCAGGCAGCTCCCGGACAATGCGGCTCTGCTGGCCCGCAACGAAGGACTCGAGGTACCCCGGTG  
CCCGGGGTTCGTGGTGCACCTGCCGATCGCACAGGTTGGCCCAACCGGCCGCTTGATGCCCGGTTCGGCAAGCCCGGC  
AGTTGCCAAACCCAGCGTGATCAGGCTCGGCTCGCGAGTTTCGGCGAAGAAGTGGCTCGCCTGATCACCTACCATCGGC  
CAGGATCTGCGTGTATCACNACGCTCGCCAAGGAGGTTGTTGTGGTGCT (SEQ ID NO. 381)

.....Rv304T7.seq:.....  
GCCACGTTTCGCGCGCGCCCGCATACGGCGGCGTACCGATCTCCGCGTCATACACCCGCGGGTAATCGCCGACGGTGC  
CGTTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAGTTCAGGTCCAGCGGGTGGCGCAGCAACGGCGCGAGCT  
CAACGACGTCAATCACGTTGTGCTTTCTACGGTCACCGACCCGGTGACCGTAGTCGCCCCGGTGGCTCGGCCGAGAA  
GTTGCACCGCCACCACCGCGACACCGTCTTGACGCGGACGCCACCCCGGATCGGTTGTTGGCAAGGTAATTGGGT  
CATTCCATTTGACGGGACGCCGACCCCGCAGCCCCAGTACCGCCACGACCACGCCGGCTGACCCACCACTGTACGA  
ACACCAAGGCGACGCCGACCA (SEQ ID NO. 382)

## Clone Rv306

.....Rv306SP6.seq:.....  
CTCAAGCTTGATGCCGCCATAAACCGAAGCGTGAGCACGCCGCCACCCACCCACGCGCGGGTTCGGGCGCCGGCCCGGGC  
CGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCCGGCTGCGCTACGTCAAGCCATACCGGGCGGA  
GCTACATCGGCTCGGCCGCCAGTGTTTCGGGCCCTCTTTCAGGTCNAGGTCNATACCGATTGCGCATCCGCGAGCCG  
CACCCTGGACGACAGAACCCTGCCCTACGAGTGCTTGTGCGGCGGGGCCAAAGAACANCTTGGCATCCTGGCGCGATT  
GGCCGGCGCGGTCTTGTT (SEQ ID NO. 383)

.....Rv306T7.seq:.....  
CTCGGTTACGCTTCGGTCGAGTGTCGAGTGATAGATGACGACCGGGACCTCGTCGGCATCTTCCATAGCCCGCCAC  
ACCTTCAGTTGCTCACCGGAATCCAACCGGTANAANGTCGGCGAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCG  
GGACGGTCAGAGCCCTCGGTCGGGCCAGCACTCCGAGGCTTCGTCGGGGTGGTCGCGACNCGCATGGGCCACCATC  
GCATTACAGGCTGTCGCG (SEQ ID NO. 384)



## Clone Rv307

.....Rv307SP6.seq:.....  
CTCAAGCTTCAATTCCTCCACGACGCGTTCCCAAATGAATTTCCCGATCCCACAATCTCGGTTAGATACAGGTCGCC  
ATACCCCTTACTTCGGCAACGCTGGGCGGATTGGCCCTGCCGCTGCAGCAAACCATCGACGCCATCGAATTGCCGGCA  
ATCTCGTTAGCCCAATCCATACCCATCGACATTCCGCCGATCGACATCCCGGCCCTCCACTATCAACGGAATTTGATG  
TCGGAGGTCGTGCCGATCGATNTNTCCGTGNACATTCCGGNGGTACCATCACCGGCACCAGNATCGACCCGATTCCG  
CTGAACCTTCGACGTTCTCAGCAGCGCCGGAACCA (SEQ ID NO. 385)

.....Rv307T7.seq:.....  
TTAACCCCCGTGGCCTCTACGCCGCTNCGGGTCGAACATGCATCCCGAGCANATGCTCGAGCGCGCACCCCACTCGC  
CGATGGCCGGAACCGGCTGGTTACCCGGGTGGCGGCTGACGTTCCGGCGGCGAGGACATCGGCTGGGAAGGGGCGCTTG  
CCACCGTCGTGGAAGACCCAGATTCTGAAGGTGTTCTGTCGTGCTCTACGACATGACCCCGCGCGGACGAGAAGAACCTTG  
ACCGGTGGGAAGGCTCCGAGTTCGGCATCCACCANAAGATCCGATGCCGCGTT (SEQ ID NO. 386)

## Clone Rv308

.....Rv308SP6.seq:.....  
CTCAAGCTTGATTTTGATCATCATGGATGATCATACCCGAAGTGTGGTAGCCGCAGTGGTTATCGTGGGTACCGTCG  
TGCTTTCCATGGGCGCCTCTTTCCGGCTTCCGTATTGGTCTGGCAGGACATTCTGGGTATCGAGTTGTACTGGATGG  
TGTTGGCGATGTCGGTGATCCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAANG  
AAATTGGGGCCGATTGAACACCGGAATTATCCGTGCCATGGCTGACCGGGGAGTGGTGACGGCTGCCGGCATGG  
TGTTCCCGCTTACCATGTCGTTGTTGTGTTACGCGATTTCGGAATTATTGGTCAGAT (SEQ ID NO. 387)

.....Rv308T7.seq:.....  
CGNCCAACCCGAATTGGTTTTCCGGCCNCTCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCGTCCGCGGGAC  
ACACCTCGATGCTGCCGCCATGGACGCGGTGGAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCCG  
CCNCGGCGTTACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCGGAGCGACGGC  
CAAGGCGGCGTGCCAGGTGCCCCGGGCGCACGGTGCGGACAAGGTGGTGCTGGCGGTCCCGATCGGCCCANACGACAT  
CGTGGCGAGATTGCGCGG (SEQ ID NO. 388)

## Clone Rv309

.....Rv309SP6.seq:.....  
CGTGACTGCCACCGGGGCCACTCCGCAGAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCCGA  
CTTTCCGCGGTACCCGCTCACTTTGTGTCNACCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCACTACTT  
CATCCTGACGCCGGAACAAATTGACNCAGCGGTTCCNCTGACCAATACGGTCGGTCCCACGATGACCCANTACTACNT  
CATTCGCACGGANAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGT  
TCAACCAAACTTGAAGGTGATTGTTAACCTGGGG (SEQ ID NO. 389)

.....Rv309T7.seq:.....  
TCGCTCAAGCGCNTGAGGCCGAANC GGCTGGTTACGACTCCCTGTTTGTGATGGACCACTTCTACCAACTGCCCATGT  
TGGGGACGCCCCGACCAGCCGATGCTGGAGGCCTACACGGCCCTTGGTGCGCTGGCCACGGCGACCGAGCGGCTGCAAC  
TGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCGACCTGCTGGCAAAGATCATCACCACGCTCGACGTGGTTA  
GCGCCGGTTCGAGCGATCCTCGGCATTGGAGCCGGTTGGTTTGAGCTGGAACACCGCCAGCTCGGCTTCGAGTTCGGCA  
CTTTCAGTGACCGGTTCAACCGGCTCGAAAAGGCGCTACANAT (SEQ ID NO. 390)

## Clone Rv30

.....Rv30SP6.seq:.....  
ATACTCAAGCTTCCGCTGGGGCCTGTTCAACCATGGCGATCCCGTTGGTCCCGGACATCCCGAACGAGGACACCGCGA  
CCNCTTCGGTGTGTGATCATTACCGTTGGGCCACTGCGTAACCGCTTGCGGCACAAAGAGCCCGGTCTCGACGTCGG  
AAAGCTCATCGGGCACCCGATTGAAATGCAGCAGCGGCGGACCAACCCCGTGCCGCGAGTGACAGAATTGCCTTGATCA  
GCCCCGACGGTCCCCGCCGATGCCGTGCTGTGCCCCATGTTGCTCTTGGCCGATCCAAGCGCGCAGGGGGTGCCCGCGC  
CATACACCCGCGCAGGCTGCGGTACTCAATCGGGTCGCCGATTGGCGTACCGGTGCCGTGCGCTCCACCACACCGA  
CCGTTTCGGGCTG (SEQ ID NO. 391)

.....Rv30T7PEG.seq:.....  
CAACAGCGTTCCAGCGGCATACACCGCACATGCCGTGCACCCGGCGCCGGGCGGAGTCGCCGCATAACACANGTACA  
CCTTGGGAATCGGTGTGCGCCAGGGATTNACCGCGGGGTGGGGCCGGCGATCGCGCGCCAGGTGAGTTGGCGCCGA  
CCGTGATNTACCCCGACGTAGTTGGCGTTGTGGTCCGCCATCCGCGCGGCGGCGACGGCGCGGGCCGCCACACGA  
TGTCACGGAAGCCGGGGCGAACGCTCGACGACCTGGTTACCGTCTCNGTCGCNTCNANCGTGGACCCGACNGCAGT

GGGCATATGTCCANAACGGACGNGGCCGTTTCNTCGATGCNGCCGGGGTCCGCGACNTGCGGACNCNCNGNCACACC  
ATCCGCCAGTCCGCGTGGCGTCCCGCCGCGACTCTGCCTCGGCCGCGCCA (SEQ ID NO. 392)

## Clone Rv310

.....Rv310SP6.seq:.....  
CTCAAGCTTTGNCGACGATCGGGCGATGTCGATGANAGGAAACCCAGCGCACAAACCGACNATTTTGGCGTAGCCGGC  
GGACNTCTGCTCGATTCCGATCACGTGCGCGCTCGCATCGAGCATGGCGCCGGCGACGGCTAGCAGCGATCCGCCGTC  
GTCGAGGAACACGACACGAGCCGTACGCCCGGCCGTAAGCCGCGCCAGGATTTCGGCGAAAAACCGTTCTACGTGGCG  
GGTGTACTGGGTGTCCAATGATTCTGTGGGTGCGTAGGCGTGCCTGCAATCGTCGACATAAATGCCGTGCGCCCGCAT  
CGCGTCAACAACTCCCGGGTGAAGTGAATANCACTTGCCGA (SEQ ID NO. 393)

.....Rv310T7.seq:.....  
TCCAACGCGGTGACAGATTTGTCTATCCTGGACCTGACGGTGAGGTGCAAGTTTTCAGGAATTCGGCAAAATCGGTA  
AGAGCCTGAAGAATTTCGGTATCGCCGGACGAAATCTGCGACGCATACGGGGCAGATACGCTTCGGGTTTACGAGATGT  
CGATGGGGCCGCTGGAGGCTTCACTCCATGGGCCACAAAGGATGTTGTGCGCGCGTACCGTTTCTGCAGCGGGTGT  
GGCGCTTGGTGTGACGAGCACACCGGCCGAAACTCGGGTGGCTGACGGCGTGGAACGACATCGATACGCTACGGG  
CGTTGCACCGCACCATCGTGGCGTGTG (SEQ ID NO. 394)

## Clone Rv311

.....Rv311SP6.seq:.....  
CTCGTCTTGACTACGCCCAGTATCGAAANCCCTCTGTGCCGGTNCGCTAAACACCCGGCGGACACTCANACGGTGCT  
GGTGGTGCGGCATGGCACCCGCGGGCAGCAAGCGCACTTCTCCGGGGACGACAGCAAGCGACCGCTAGACAAGAGGGG  
TCGTGCGCAGGCAGAAAGCGTTGGTACCACAGCTGCTGGCGTTTCGGCGCCACCGATGTTATGCGCGCCGACCGGGTGC  
CTGCCACCANACNATGGAGCCACTCGCCGCGGAACTGAACGTGACCATACACAACGAGCCNCCTGACCGAAGAGTC  
CTACGCCAACACCCCAACGCGGGCGACACCGAGTGCTGCAGATCTTCG (SEQ ID NO. 395)

.....Rv311T7.seq:.....  
GTATCGCTCCNCCTTTGGCCACAGCAGCCACAGCGGTTTCGCGGACCGAACGTGGACATCAATAGCCCGGAATCG  
GTGTGTGCAAGTTGGTAAACGGTGTGATCCCAAGCTTTGCCAGCCTTTTCGTAGTCTTGGGCCCCACACCCACAGT  
GCTTCGACGGTACGGTCACCCATGATGGCCATCCAGTTGGCATCGGTGAGCTGATAGATGCCAGCTGGTTTCGCCAAC  
CCGTAGCGATCTTGGCGCGCTGCTTGTGTCACTGATACCTATCGAGCAAGACAGCCCGGTTTTCGACAAGATGACT  
TTTCGGATCTCTTCNGCGAACTTCCAATGGGGGTCTCCGGGANT (SEQ ID NO. 396)

## Clone Rv312

.....Rv312SP6.seq:.....  
CTCAAGCTTTTGGTCTAGCCGGCCGAGCAGATACGGGTGTCCTTGGCCACCGGCGGCGGCTGTCCGGGAAATGGCGG  
GTCCCCGGTGGTTTTGCTGANGANTGCTGAACCGTAGTCGAAGTGGGCGGCGTCAGACTCCACCCAGCCAGCAGGCAG  
CGCGAAGCTGAATCCTCAACCGGGTGTGATCCGGACAGGTTGGGGTGCCTTGGGGCAATGACAGGTGGCGGCGG  
TGCGTTTCGGGTTCGGCCGGCGGAGGTGCTGCGTTGGGATCNCCTGGCTGGGCATTTCGCNTNTTGGCGGCGGCGGTG  
TGGGGGGGCAACANGTGTCCCGGTGCGGGTGGCGCTGC (SEQ ID NO. 397)

.....Rv312T7.seq:.....  
ATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCCGACTTTCGCGGTACCCGCTCAACTTTGTGT  
CGACCCTCAACGCCATTGCGGGCACCTACTACGTGCACTCCAATACTTCACTCCTGACGCCGGAACAAATTGACGCAG  
CGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACTACATCATTGCGACGGAGAACCTGCCGCTGCTAG  
AGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAACCAAACTGAAGGTGATTGTTAACC  
TGGGCTACGGCGACCCGGCCTATGGTTATTGACCTCGCCGCC (SEQ ID NO. 398)

## Clone Rv313

.....Rv313SP6.seq:.....  
CTCAAGCTTGCAATGCGGGTTCGGGATGCCCATGGTTGGAANATGGTCGCCCTGGCGTCNAATACGCGCGAGCGCATGA  
GCTACCGGTTTCGGAACAACGTATCGAAAAACGTGCGACTGCTGGCAGATGGTATCTCCGATGTGGTTGTAATTTGTA  
TCCCAACTCTAACTGTGCTATCGGATCAGCGTGAATATCGANATATTGCGAATGCGATGACAGGCCGCCATTCCGTTT  
ATTGCTTACGCTTCCCGGGTTCGATTCTGTGACTGCCGCAAAACGCGGATATGATTGTTGAAACCGTATCTA  
ACGAATTATTGATGTGGTAGCGGCAGCTGCCGTTTTGTGCTGTCG (SEQ ID NO. 399)

.....Rv313T7.seq:.....  
CAAATACACGCCGGACGCACAGGCGGACATCGCCATCCCGAGCACACCCAAAACGGGATACAGGATGGAGGCCAACGC  
CACGGCCGCGCCAGGATCACCAACCACACCGGCTTGGTCAGCTTGTGCGCGCGGTATAGGCATCGGGCCGCTGCAA  
CGCAGCATGCACAAACGCGTACACCGCTGTCACCAAGACGGCGACCAGCAATACCAGCATGACGGTACCCACGAGGTG  
GCTCACGCATTACAGACTATGCGGTTTGCATCCAACACG (SEQ ID NO. 400)

## Clone Rv314

.....Rv314SP6.seq:.....  
CTCGTCCTTCGGCCTCGCTGCAGGAGTGGGAGCCGCAGGGCTGGAAATCCGAAAAACGAGCCGGTGATCGCACTGTGCG  
CCGATCGGCGCCGCACCTGGTTGGTGTACGGATGAATCCGCAGCGAAATGTGGCTGCGGTGGCGTGTGCTGACTCGT  
TGGCGTCGACGCTGGTGGCAGCCACCGAGCGGTTGGTCCAGGATCTGGATGGGCAAAGTTGTGCGGCCCGGCCGGTGA  
CGGCCGATGAGCTGACCGAGGTGACAGCGCCGTGTTGGCTGACTTGGAACCGACATGGAGTGCAGCCCGGTT  
(SEQ ID NO. 401)

.....Rv314T7.seq:.....  
GTCTAGNCCGCGAACACGATACGGGTGTATTGGCCACGGCGCGGCTGTCCGGGAAATGGCGGGTCCCCGGTGGT  
TTTGCTGAAGANTGCTGAACCGTAGTCGAAGTGGGCGGCGTCAAGTCCACCCAGCCAGCGAGCGCGAAGCTGAA  
TCCTCCAACCGGTTGTGATCCGGACAGGTTGGGGTGGCTTTGGGGCAATGACAGGTGGCGGCGGTGCGTTCCGGTC  
GGCCGGCGGAAGTGTGCTGCGTTGGGATCGCCCGGCTGGGCATTGCGCGTGTGGCGGCGCGCGGTGG  
(SEQ ID NO. 402)

## Clone Rv315

.....Rv315SP6.seq:.....  
ACTCAAGCTTGAGATTGGCGTCAACGGGTGTGCGCACCGGCGTCTGCAAGTGGTAGGCCTGCAGTTTGTGCATCAGG  
CCGATGCCGCGGCCCTCGTGGCCACGCATGTACANACCCACGCCGCGCCCTCACGGGCGACCATCGCCAGCGCGGCG  
TCCAGCTGAGGCGCCGCAATCGCAGCGGCGTGACCCAAACACATCGCCGGTCAAGCACTCCGAATGCACCCGGACACG  
ACGTCG  
TCACCGTCCGCGTTGGGCCCCGGCGATCTCGCCGCGGACCAGCGCGACATGTTCCACGTCTCTCGTAAATGCTGGTGTAN  
CCGATGGCGCGAAACTCCCCATGACAANTCGGAATCCGCGCCTCGGCGACCCGCTCAATGTTGCTTCTCNTGCTTG  
(SEQ ID NO. 403)

.....Rv315T7.seq:.....  
TCGACNAGCATTCTTGACNGTTGTTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCCACCAGATCATCTTGGTC  
CGGTAGCGCTCGTCCGGGTATGCTGCCGCGGGGATTCTCGCTGCTATTACTCCCCCGAAGAACGCCACCGGTCCAGC  
GCGTGGGCGCGCGGTTCCCATCACAACTGAACCCCCAACAGGGGACATGCTTAGCGGTAGGGCGCGCGCAAGGC  
GGCAGCAATCGCATCACTGCGCTGCGCGTCACTATTAACCCACCCGACTTCACTTCCACGACCCCGAATGGCGCCCC  
GTCATTGATCATCTTGCGCACCGCGGATAATCCGGGAT  
TG (SEQ ID NO. 404)

## Clone Rv316

.....Rv316SP6.seq:.....  
ACCGGGGGCACTCCGCACAATCTGTACCCGACCAANATCTACACCATCGAATACGACGGCGTCGCCGACTTTCCGCGG  
TACCCGCTCAACTTTGTGTGNACCCTCAACGCCATTGCCGGCACTACTACGTGCACTCCAACCTACTCATCTGACG  
CCGGAACAAATTGACGCGCGGTTCCGCTGACCAATACGGTCGGTCCACNATGACCCANTACTACATCATTCGCACG  
GANAACCTGCCGTGCTAAAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAACCAAAC  
TTGAAGGTNATTGTTNACCTGGGCTACGGCGANCCGGCCTNTGGTTATTCCACCTCNCCGCCAATGTTTGCNACTCC  
CGTTCCGGGGTTGTTCCCNNAAGGTCAACCC (SEQ ID NO. 405)

.....Rv316T7.seq:.....  
CGCTCAAGCGCNTGAGGCCGAANC GGCTGGTTACGACTCCCTGTTTGTGATGGACCACTTCTACCAACTGCCCATGTT  
GGGAGCGCCGACCGAGCCGATGCTGGAGGCCTACACGGCCCTTGGTGGCTGGCCACGGCGACCGAGCGGCTGCAACT  
GGGCGGCTTGGTGACCGCAATACCTACCGCAGCCGACCTGCTGGCAAAGATCATCACCACGCTCGACGTGGTTAG  
CGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGTGGTTGANCTGGAACACCGCCAGCTCGGCTTCGAGTTCGGCAC  
TTTCAGTGACCGGTTT (SEQ ID NO. 406)

## Clone Rv317

.....Rv317SP6.seq:.....  
CTCAAGCTTGGTTCGATGAAGTAGTCGTCGGTCAGCGCCGCTCTTCGAGCTCCTTGGCGATGCCAGCAAGGAGTC  
ATCGCGCGGCTTGGCCAGGATCTTGTGCGGCTTCTTGGACGATGCGGGCCCGCGGATCGTAGTTCTTGTAGAC  
ACGATGACCGAAACCCATCAATTTGACCCCGGCTCGCGGTTCTTGACCTTGCGTACAACTCGCTGACGTCGTGCGC

GCTGTGCGGAATGCCCTCGAGCATCTCCAGGACAGCCTGATTGGCGCCGCCATGAAGCGGACCCCATAGTGC GTT GAT  
GCC (SEQ ID NO. 407)

::::::::::Rv317T7.seq::::::::::  
GGTCAGGCCGAGCAGGCGCGAGGAACGACGAACCAACAAGCCATGGTGGTTGGCGCCGTCGAGAGGTGGCGGTCGC  
CACAACGGGAAGATCGCCTTGAGCGTCGCTCGACCGCCGCCTCGAGTTGGGTCATAACGAAGTAGCTGATGCCGATCA  
TGTCGACGTTTCCGTCGCATCAGCGTGCAGCGGCGACCCACTCNACGAGGTCTCGGTGCCGCGCGGGCCAGGGCACCA  
GCAGTGACGAGTCCAGGCGCCGTCGGGCCAAGCAGTCGCGGTGCCANCCGTGGTGGGTCGGGCGATGGTTGGGTGTGC  
TCATTTCCGGGAACGCCA (SEQ ID NO. 408)

Clone Rv318

::::::::::Rv318SP6.seq::::::::::  
CTCGAAGCTTTAACAGCATCAACCCCGCCCGCACCAGCACCGACACNATGTCGATGCCATCGAGGTGAATGTGGAAC  
TGGCGCAAACCATCGGCGACCGCGACCAACCGGCAACATGGGTACCGGCGATTTCCGGTGCCAATGCCGACCGGACGGG  
CCGCTCTCACCAGGTGACCTCGATCACCAGACCANCCGGCCGTTNTNNTCACGCACCCCTACCGTGTACGCCCA  
AAACGGCGCTGGTGGTCGATTGCCGGAGTGACCCCNACCCAGTGTCTGTCGCGGATCC (SEQ ID NO. 409)

::::::::::Rv318T7.seq::::::::::  
TGATGCCGACCCGATCGACGGTCGTTGGTCGGGGTTGACTGGCCGCCCGGCGAAGCAGGGCGTCGACCGCGGCCCGG  
ACGTCCGCGGCCGTCACCGGTCGGCCATTGCCCGGGCGGGAGTCGTGAGCTGACCACGGTAGACAAGTCGGCGCTGG  
CCGTGGAAGACNAACGTGTGCGGTGTGCAGGCCGCGGAGAAGGCGGGCGACNTCTTGGGTTTCGTCTANAGATAC  
GGGAACGTCCAGCCGTGGCGGGCGGCCCTCGGCGACCATCTGATCGGGCCCGTCC (SEQ ID NO. 410)

Clone Rv319

::::::::::Rv319SP6.seq::::::::::  
TTTCGGGCGAGGCGGTATANCTTCCNCTCGTACCGGCGACCGCCAGCCGANAAGCTCGTTTTCCAGTGTTGCTGGGG  
ATTCTCACGCTGCTGCTGANTGCTGCCAAACCGCTTCCGCTTCGGGTTACAACGAGCCGCGGGGCTACNATCGTGCG  
ACGCTGAAGTTGGTGTCTCCATGGACTTGGGGATGTGCCTGAACCGGTTACCTACNACTCCAAGCTGGCGCCGTCT  
CGTCCGCAAGTCGTTGCTTGCGATAGCCGGGAGGCCGGATCCGCAATGACGGATTCCNTGCCANCGCTCCGAGTTGC  
NTGCGGATCGACTACNAATTGATCACCANAAACCATCGGGCGTNTTACTGCCTGAAGTACCTGGTGGGGTCGGATAC  
TGCTATCCGGCGGTGACAACCCCGCAAGC (SEQ ID NO. 411)

::::::::::Rv319T7.seq::::::::::  
GTTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCCACCAGATCATCTTGGTCCGGTAGCGCTCGTCCGGGTATG  
CTGCCGCCGGGATTCTCGCTGCTATTACTCCCCCGAAGAACGCCACCGGTCCAGCGCGTGGGCCGCCGCGGTCCCCA  
TCACAACTGAACCCCAACAGGGACATGCTTAGCGGTAGGGCGCGCGCAAGGCGGCAGCAATCGCATCACTGCGCT  
GCGCGTCACTATTAAACCCACCCGACTTCACTTCCACGACCCGAATGGCGCCCGGTCAATTGATCATCTTGCGCACCG  
CGGATAATCCGGGATTGCCAGCCCATTCNACTACCGCATGCGAGTCATCGGCTGACCGCAGCGGTC

(SEQ ID NO. 412)

Clone Rv31

::::::::::Rv31SP6.seq::::::::::  
TCGCCTAGGCGGGCTTCCCCTTCCGTCGAGCNGTCAGAAGCTCCTATGACAATGCACTACCCGAGACNATCAACGGC  
CTATGCAATACCNAGCTGATCAAACCCGGCAAGCCCTGGCGGTCCATCGAGGATGTGAGTTGGCCACCGCGCGCTGG  
GTGCACTGGTTCAACCATCGCCGCCTCTACCGGTACTGCGGCGACATCCCGCCGGTCTAACTCGACGCGCGCTCACTA  
CGCTCAACGCCAGAGACCANCCGCCGGCTGACGTCTCAGATCAGAGAGTCTCCGACTCACCGGGCGGTTTCATCCCC  
ACTGTGATAGCGTCTGTGGATAACTTTGTCTGCA (SEQ ID NO. 413)

::::::::::Rv31T7.seq::::::::::  
GCGCGTNGAACTGATAGGTGCGGCCCGGCTCGAGCANGCCGGCCATTTGTTGATGCGGTTACCGAAGATCTCTTCGG  
TGACCTGCCCGCCGCCGCGGAGCTCGGCCAGTGCCCGCGGTTGGCCGCCGCGGCGACAATCTTGGCGTCCACGGTGG  
TCTGGGTCA (SEQ ID NO. 414)

Clone Rv321

::::::::::Rv321SP6.seq::::::::::  
CTCAAGCTTCAATACAGAGTTATAAACTGTGATAATCAACCCTCATCAATGATGACNAACTAACCCCGATATCAGGT  
CACATGACGAAGGAAAGAGAAGAAATCAACTGTGACAAACTGCCCTCAAATTTGGCTTCCTTAAAAATTACAGTTC  
AAAAAGTATGAGAAAATCCATGCAGGCTGAAGGAAACAGCAATAACTGTGACAAATTACCCTCAGTAGGTGAGAACA

ATGTGACGAACCACCCTCAAATCTGTGACAGATAACCCTCAGACTATCCTGTCGTCATGGAAGTGATATCGCGGAAGG  
AAAAAT (SEQ ID NO. 415)

## Clone Rv322

.....Rv322SP6.seq:.....  
CTCAAGCTTCGATCGACATTACTCCCGCCTTGGGTCTGGTCTCCGAGCTGGTTCGGTTCATGGTTCGGACCTGCTGGTAGT  
GGGGATCTAACGCAACATGGTGGGATTCATCATGGTGTACCCGTGATACCCATTCCGAGCTGCCGGTGAAACCCCGC  
GATGCCGGGATTTCCAGCCGCACTAGGATGTCTAGCCGGCCAGCCGTGCCGCCGACTTCGGGATGTTCCGGTATACC  
ANCGATCGGCAATCTTGCGTATCCGCCGATGCTCGAACGCTANCCACGCCAAACCAACCACTGTGACNACAATCGCCA  
CCACACCAAAGGTCATGCCCTCGGCGTGATGTCCGGTGCCGAAAGCCGCAAGAGCTCCGACGCCGCC

(SEQ ID NO. 416)

.....Rv322T7.seq:.....  
CATTCCCAATTGAATTTCCCNATCCCAATCTCGGTTTCAGATACAGGTTCGCCATACCCCTTACTTCGGCAACGCTGG  
GCGGATTGGCCCTGCCGCTGCAGCANACCATCGACGCCATCGAATTGCCGGCAATCTCGTTTCAGCCAATCCATACCCA  
TCGACATTCGCGCGATCGACATCCCGGCTCCACTATCAACGGAATTCGATGTCCGAGGTCGTGCCGATCGATGTGT  
CCGTTCGACATTCCGGCGGTACCATCACCGGCACAGGATCGACCCGATTCCGCTGAACTTCGACGTTCTCAGCAGCG  
CCGGACCCATCAACATCTCGATCATCGACATTCCGGCGCTGCCGGGCTTTGGCAACTCGACCGAGCTGCCGTCGTCGG  
GCTTCTTCAACACCGGCGGCGGTGGCGCT (SEQ ID NO. 417)

## Clone Rv327

.....Rv327SP6.seq:.....  
CTCAAGCTTTTCGGCGGAGACGGACANNTTGCGAACATTGATGACAAAATAGAAATCATTGATGGTTTGAGTCACCAGG  
CCGATCAAGCCTTCGCCGAGCCAAATTCGAATCAAGAGGCCCAAGCCCGTACCAATCAGCCCGGCAACGAGGGATTCC  
GTCAATTACGCCAAAATAACTGCTCTCGGGTTACACCCAAACAGCGCAATATGGCGAAAAACGGTCGCCGTTGCACG  
ACATTAAATGTCACGGTATTG (SEQ ID NO. 418)

.....Rv327T7.seq:.....  
AGCTTAACTGCTCCCTAATACCTGGGGCTGTGCCTGCGGTGTATGCACGGCATAACGGACATCCNTCCCCTGAGACCCN  
CGGTCTAATCAGCCACGTGTCCACCATCAGGGGTCAACCCCGGCCAAGGGCGACGGCACCCCAAGTTCGCCGACCGTT  
AACCTATTGCTGTGAGCTTCATTTGCTGCGAGCAAAACAGTTGGTCCGCCGTTAGGAACTGAATTGACACTCAACCGA  
TTTGGTGCCNCCGTAGGTGTCTGGCTGCGGGTGCGCTGGTGTTCGCGGTGTGGTAACGACCACAATGTGACCGGG  
GGAGGTGCAACCACTGGCCACGCTCCGCGAATGTCTATTGCGGGG (SEQ ID NO. 419)

## Clone Rv328

.....Rv328SP6.seq:.....  
CTCAAGCTTGGGGTGGCGCTGTCCGTCGGTGTGCTTGGCGCGCTCGGTATCAACACCGCCACGAAATGGGGCACAAG  
AAGGATTTCGCTGGAGCGGTGGCTGTCCAAAATCACCTCGCCAGACCTGCTACGGGCACTTCTACATCGAGCACAAC  
CTGGGCCATCACGTCCGGGTGTCCACACCGGAGGACCCGGCGTCCGGCGCGGTTCCGGCGAAACGTTGTGGGAGTTCCTG  
CCCCGAGTGTATCGGCGGCTTGCCTCGGCCGTTTCAATTTGGAGGCCCAACGGCTGCGTCGGCTCGGCGTCAGCCCC  
CT (SEQ ID NO. 420)

.....Rv328T7.seq:.....  
GCACCAAGGCCCCACACGTCAACCTGTGACCTCCTGCGCCGACCCCGCCGAGGTCCTGGCCGTTACCACTGAACGG  
GCGAGCCGGGAGTCTGGTACGCATCGAACAAAGAGCAAGGTGCATGGGCGGAGTTGTTCCGCCACTTCGTTCGATGACG  
GGGTCTNATCCATTTCGAGGTCCGTGCGCGCTCGGTTCGAGTGGCGGTCACTCCAGGTACTCGACCTCACAGACGAGA  
GGACTCGATCCCATCTAGGTGTGGACGAAACAGATCTTCTGTCCGA (SEQ ID NO. 421)

## Clone Rv329

.....Rv329SP6.seq:.....  
TCGCCTCCGCATATGGGTCGACGCCAAGCGGGTCCGGATTTCTGGGCTTCATCGCTCGCGCCGTCCGCGACAAACAGCG  
CGGTGCAACCGACACTCGTTGTGATGTCCAGCTATCACCTTCGGTACGCACCCAATCGACCCCTACNCGGCTATCTCA  
GCCGCGATCTCCAGGCTCCGCCGAGCCAGGTGCATCCCGGTCCGGATCCCACTAACCAGGACCATTTGGCGTCN

(SEQ ID NO. 422)

.....Rv329T7.seq:.....  
GTCCTCGAGTGCCGCCGTTCGNACNCCCAGCGCCCGCGGCCACTTGGATGCGACCCGTTTCAAGTCCCTTCATCAT  
TTCGCAAAAGCCTTGACCATGGCTCCGCCAGGATCGCCGAGACCGGACCCGGAGGTTGTGCAACGACAGCTCGCA  
GGATTTCGACGCCCTTGTAACCCAATTCGGCAAGTCCCGCGACACCGTGAGTCCCGGCCGGGTTTCGACGAGCAGAT  
CGACATGCCTTGGTGCCGCGGTGTGGCGTTCGGGTCGG (SEQ ID NO. 423)

## Clone Rv32

.....Rv32SP6.seq:.....  
GGCATACCAATGTGGACTTCTGCTCACCACGATATCCGTGGTCTGATCCGCTGCTGCGGCGGGCTGCNACCTGCNTC  
TCNGCGGCACCCGTNACTACATGGCNCGCGCCGACGCATACGTGCGGCGGGGACCCACTCCNACTGGTCGACGGTGC  
TGGCCGCGTGTCCGCANGTCCNAACCCGCGCCGACCGACGAAACCGGCCGCGTCCGTTCTGGACCAACGCTCATGT  
GCCGTGCGGGTCCATGCTCGACGCCATCGAGACCGTAACCGAGCGTCTCGAGCGGTTCCGCTCCGGCTTCCGTGACAT  
CTTCGTGGTCTGCTGCGGCCGTGCCGCCGCGGGATGGTCCGACCACAACGCCAACCACTCGGCGGTGACATACCCGTC  
CGCGCCACTCGACCTGGCGCGCGATCGCGGCC (SEQ ID NO. 424)

.....Rv32T7.seq:.....  
GTGAGCAGACCTACGCCNCCTGGTTGCGCAACTCGGTACCGATCATGGCGCGCNGCCTGTCTGTCACCGATACCCAGC  
GAACAAGACAGCCCGGTCCGCGACAAGATGACTTTCCCGATCTCTCGGCGACTTCCATGGGGTTCGTCGGAGTCCCG  
GGCGCCACCGCGAGGTAACCTCGTCTCAGTCCCATACGCGACCGGGTATCCACGTGCGGCAACAACGCCACCACTC  
CCAGACGCCNCGTGTACGCGGCTGGGTTCCACNGCAATAAGTGGCCTCANGGCATCGTCCGGCGCGGTCCNCAAC  
GCA (SEQ ID NO. 425)

## Clone Rv330

.....Rv330SP6.seq:.....  
CTCAAGCTTGAGGTTAACTTTGAACGGATCGAGCTGGACGTTGAGACGGTGATCGGGCCGAACCTGAATTGTCCGGT  
AATGCCAACGCAAAAAGCAGGGTGGTGGCCGGGGCGGTGAAACCGGCGTCGGCGGCACCGTCGAAATCTATGTGGAT  
TGCCGGAATGGGGATGTCCGGCACGGCGAAACCGTAGTTGCTTGTCCCGTGAGGCCAGGTGGATGGGGGAAAGAT  
CCTGGTGTCCGGGATAATAATGGGGCCGATGCCGCCGGTTGAAGTCCACTGGATCGGGAATCCGGAATCTTGATCCG  
ACGTTCAAGCCGAACAGGCCCTC (SEQ ID NO. 426)

.....Rv330T7.seq:.....  
CGGCGACGTCGCGATACGCCGAGCAGTTGGGAATCGCTCTGCGACAAACCAATATTCTGCGGACGTTGAGAGGACT  
TTTTGAATGGACGGATCTACCTGCCGCGGACGAGCTGGACCGATTAGGCGTACGCCCTCCGCCTGGACGACACCGGGG  
CACTCGATGACCCGACGGACGGCTCGCGGCNCTGCTGCGGTTCACTGCCGACCGCGCCGAGACTGGTNTTCGCTGG  
GACTGCGGCTGATTCCACACCTCGACCGCCGACGCGCTGCCTGCTGTGCGGCCATGTCTGGCATCTACCGCGTCA  
TCGCCCTTGATCAGAGCATCGCCGGCGGTCTGCTA (SEQ ID NO. 427)

## Clone Rv331

.....Rv331SP6.seq:.....  
CTATAAAATACTCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACCACGCGCGGGTCCGGCGCCG  
GGCCCGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCGGNTGCGCTACGTCNAGCCATA  
CCGGCGGAGCTACATCGGCTCGGCCGCCAGTGTTCGGGCCCTCTTTCGAGGTCNAGGTCNATACCGATTGCGCAT  
CCGCAGCCGACCCCTGAACNACANAACCGTGCCCTACTATTGCTTGTGCGGCCGCAAAAAACAGCTTGGCATCCT  
GGCCNATTGGCCGGCGCGG (SEQ ID NO. 428)

.....Rv331T7.seq:.....  
CTTCGTGCGAGTGTGCGAGTGATGACGACCGGGACCTCGTCGGCATCTTCCATAGCCCGCCACACCTTCAGTT  
GCTCACCGGAATCCAACCGGTAGAAGGTCCGGCAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAG  
AGCCCTCGGGTCCGGCCAGCACTCCGCAGGCTTCGTGCGGGTGGTCCGACGCGCATGGGCCACCATCGCATTACCA  
GGTCTGCGCGAATCNCANACGTANACNCTTCTTCTAA (SEQ ID NO. 429)

## Clone Rv333

.....Rv333SP6.seq:.....  
CTGGCACCAAGGCCCCACACGTCACCCCTGTGACCTCCTGCGCCGACCCCGCCGAGGTCTGGCGGTTACCACCGAAC  
GGGCGAGCCGGGAGTCTGGTNCGCATCGAACAANAGCAAGGTGCATGGGCGGAGTTGTTCCGCCACTTCGTGATGA  
CGGGGTCNATCCATTGAGGTCCGTGCGCGCGTCCGTCNAGTGGCGGTCACTCCAGGTAATCGACCTCACAGACNA  
AAGGACTCNATCCCATCTAGGTGTGGACNAAACAGATCTTCTGTCCGACNACTACACCACCCAGGCCATCGCCGC  
CGCCCGGATGCCAACTTCGACGCCGTACTGGCCCCGGCGGGGGCGCTCCCGGTTGTCAACACTTGCCGTGTTCT  
TCACGCNCTGCCCCACATCCAACCCCAACG (SEQ ID NO. 430)

## Clone Rv334

.....Rv334T7.seq:.....  
GTTCTTGGGCCCATGCGGAGGTATCGCCGTTTCCACCACGCGGTGCGGGTGGCGTTGCATTAGCTCACCGATGGTGCG  
CTTGTGAGGCCCGCGGGATACCCCGAGTGCCGGTAAACCATCTTGTGCTGC (SEQ ID NO. 431)

## Clone Rv335

.....:Rv335SP6.seq:.....  
CAATACTCAAGCTTGGCGTGCCGTTCCAACCCGAATTGGCTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTCA  
ACNACNACGTCGTCCGCGGGACACACCTCGATGCTGCCCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTAC  
AACGCCGCGCGGAACGCTTCCGCCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATC (SEQ ID NO. 432)

.....:Rv335T7.seq:.....  
CNTCATGATGATCATCACCCGAAGTGTGGTAGCCGAGTGTTATCGTGGGTACCGTCGTGCTTTCCATGGGCGCCTC  
TTTCGGGCTTTCCGTATTGGTCTGGCAGGACATTCTGGGTATCGAGTTGTACTGGATGGTGTGGCGATGTCCGGTGT  
CCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCTGGTTGAAAGAGGAAATTGGGGCCGGATTGAA  
CACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTGACGGCTGCCGGCATGGTGTTCGCCGTTACCATGTG  
GTTGTTTGTGTTACGCGATTTCGAATTATTGGTCAGATCGGTACCAC (SEQ ID NO. 433)

## Clone Rv336

.....:Rv336SP6.seq:.....  
ATACTCAAGCTTTTACGGTGATCGCNCATCAGCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCGGCA  
ACATGAGCCAGCCTCTCGTCGGCGGTTCGGGTGCAGGTGCTCGGGCAGCTCGGCCGCNACAGCCGCCTGACCCTGAAAC  
CAGCTTCCATATCCCGCGANNAACGACGCCAGTCCGCTACGTNACCCCTCCGCGACTGTCCATGGACAACAGCGCGTT  
CTCCACCGACCGGGCCGGGTGTGGGGTNTT (SEQ ID NO. 434)

.....:Rv336T7.seq:.....  
GCTGGTAGAGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTCGGCGGCTACGTGCCATCGAGACACTGGC  
GCAGGCTATCGCACCCGTTATCGGCTACGAGCAAATCGCGGTATGCGTTCTTGAGCATGAGTCGGCGACCGTCGTCAT  
GGTCGACACCCACGACGGAAGACGCGATCGCCGTCAAGCATGTGTGCCGCGGATTATCAGGACTGACCTCCTGGCT  
GACCGGCATGTTTGGTCGCGATGCCTGGCG (SEQ ID NO. 435)

## Clone Rv337

.....:Rv337SP6.seq:.....  
GCTTTCCGCCGATACCCGCCATGTCNCGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGGCGGGATCCCAAAG  
TGCGGATGATCGGGCCGCCCTACGTCGTGGTGTACCTCGTCGGTAACAACGAAACCGAAGCGTATGACTCGGTCCACGC  
GGTGCGGCACATGGTGGACACCACCCGCCACCGCGGCGGTTGAAGGCCATGTACCCGGTCCGGCANCACTCAATGC  
CGACAGGCCGAGGCCGGANACAAAANTATCGCTAAGGTCACCGCGATCACNAGCATGGTGATCGCAGCAATGTTGCT  
AGTGATCTATCGCTCCGTAATTA (SEQ ID NO. 436)

.....:Rv337T7.seq:.....  
CTTCCAACCCGAATTGGCTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCGTCCGCGGGAC  
ACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCCG  
CCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCGGAGCGACGGC  
CAAGGCGGCGTGCCANGTCGCCCGGGCGCACGGTGCGGACAAGGTGGTGCTGGCGGTCCCGATCGGCCCA

(SEQ ID NO. 437)

## Clone Rv338

.....:Rv338SP6.seq:.....  
TACTCAAGCTTCGCGAGATCCGGATGGCACTCACGCTGGACAAGACCTTCACAAAATCTGAAATCCTGACCCGATACT  
TGAACCTGGTCTCGTTCGGCAATAACTCGTTCGGCGTGACGAGCGCGCGCAAACGTNCTTCGGCATCAACGCGTCCG  
ANCTGAATTGGCAGCAAGCGGCGCTGCTGGCCGGCATGGTGCAATCNACCAGCACGCTCAACCCGTA

(SEQ ID NO. 438)

.....:Rv338T7.seq:.....  
CCCACGACTTCTCCTCGATCAGTTGGATTTGTACGAAGAGGCAACGAAAGCAGTGATCCTCGGGATGGTTCGACGCCT  
ACATCGACCCGCCGTTACGCCGCACAGCCTGTAGATGCGCTGGGCGAGCAGGTCCACAGTTCGCCCGCTAAGGCAC  
GGCGTCTGTTCCCGTCCGGATCGCCATTCCGGCTCGGCGTCTGCTCCCATTCGATCAATAGGGCTGGCAGCTCCGTC  
GGCAGGGGCTACGCTCACCCGTCAG (SEQ ID NO. 439)

## Clone Rv339

.....:Rv339SP6.seq:.....  
CTCAAGCTTATGCGCGCCGGCCGAGGTCTGCTCACGGCAACCCCTGAAGTTTAGGGGACNACCTACTCAGCGCAAAAT  
TTCGCTAATGTGAGTCCGCCCCACCAGGGGNANATCAACCCATGTGATCATGATCTACCCGGATACCGGATTGGCGG  
TAGCGCCACGATCGTCNAAATNTCCGCTGAATCATCGGATAGCTGATCCGGCGTCAACGCGTTTTGANTTACCGC  
GCAACAGCCGCCAGGCCGGCCGCCANCGANCCGATCTCNTCGGGCCGCGATGGGCCCAATCTTNTCG

(SEQ ID NO. 440)

.....Rv339T7.seq:.....  
GTGTGTGGTGGAAACCATCTGAGCAGTGTGCCAAACCGGGGACAGACAGCTCCCAATTGACGTGAGCCCGCTCACTTGC  
TGGGTAAGCGTC (SEQ ID NO. 441)

## Clone Rv33

.....Rv33SP6.seq:.....  
CTTTACACTTCCTGCATCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATG  
ACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGGGCGTGACGGCCACCGGGGCCACTCCG  
CACCATCTGTACCCGACCAAGATCTAC (SEQ ID NO. 442)

.....Rv33T7.seq:.....  
CAGGCATGCAAGCTTTAGCTGCCCCGAATGCGTCACCCCGATGCGCCAGATCGGGGCTTCGCAGATAAAGCACGAACA  
GGCGGGCAAAACGTCNATCTCGGAGCCGGAAGGGCAATCAGCCGACCGTCGACGAACGACACCGGCGAGACCACTTAG  
GCAGTGACGGCCGGCCGAACATTACGCGCTCGTTGATTAGGCGTTGCGTCTCGTCCGCGGTGCTGCCGAGCAGCTTG  
CGGCAGATCTGAACGCTGTCTGTCCGGGACGCGCGCCGGGCGTTGGGGTGCTGCCGAATGTGACGAAACGGAGC  
CGGACCCGTCTCGGCGGGCCGCGGACGGCGATCCGC (SEQ ID NO. 443)

## Clone Rv340

.....Rv340SP6.seq:.....  
CNCAAGCTTGCGGATGTTACCCCTGACAGCCTGAACTATGTGNAAACACACGGCACCGGAACGGTGTGGGGGACCCC  
ATCGANTTCGAGTCGCTGGCGGCCACTTATGGCCTGGGTAAAGGCCAGGGCNANAGCCCGTGCGCATTGGGGTGGTGC  
AAAACCAACATCGGCCACCTGGAGGCGGCCGCGGTGTGGCTGGATNCATCAAGGCGGTGCTGGCGGTGCAACGTGGG  
CACATTCCCCGCAACTTGCACTTACCCGGTGGAAACCCGGCCATCNACGCGTCGGCNACGCGGTGTTCTGTCCNACC  
NAAACCCCCCGTGCCCGGCGGC (SEQ ID NO. 444)

.....Rv340T7.seq:.....  
GGAACCGGTAACCAGATCAGCTCGTCGACCTCACTGCCGGGGTGAATTCCCCACCGGTGCTGCGCGCTGCCAGTAG  
TGCACCTTCTTGACGCTCGAAAAGGGGAGTCGGTTCGGGTAGGTCACCGTCAGGAGCCGCTACCCAGGTTGGCGCNA  
TAGCCGGTCTCCTCGAGTATCTCCCGCACCGCCCCACCGGTGCGGTCTCACCANATCCACTTTGCCCTTGGGCAGC  
GACCAGTCGTCGTANCGGGGCGGTGAATGACAACGATCTCGACCGGCCCTTCN (SEQ ID NO. 445)

## Clone Rv341

.....Rv341SP6.seq:.....  
TACTCAAGCTTCAGAACAGGCCTGTTGTGGGNCACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAAGTGCGGCC  
GCACCGCCGGCATCTCCCGTACGCAGGGCCGCGCCGCGCGCAGCGACGGCGTGTTCGCGCAGTTCCGCGTCAA  
TGATGCTGACCTGATCGGCCACCGGGCGTTCTCGGCGTCTGCGGTTCACTAATCGCGGTGCTCAGCAGCGTCTCGA  
CAGCCACACCCGAGTGGCGACCACTGC (SEQ ID NO. 446)

.....Rv341T7.seq:.....  
TAATGTCTTGCCAACGTCAACACAATCGCGATGAATTCAATCATGCCGCCAGGGCGGCCAACCAATGGTGGCCGCG  
AGCGGCAGCTCGATCGCAGCGCGGAGGTTGCCGGCCGCCAGTTGATTACGAACAGGGTGAGGTATAGGCGGGCAGG  
ATAGTGACGAAGGCAAGACCTATATCTGCCGTGGAAGAAGAATCGAGTAGCCGGTCGACACAACGGAAGCGAAAGTG  
TCCGCGATGTTGATGAGCGTCGCCGTTGTGGCGGCGGTGGCGGC (SEQ ID NO. 447)

## Clone Rv343

.....Rv343SP6.seq:.....  
TACTCAAGCTTTCTGTCAGTTCATCGCGCCAGCAGACCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGGCCAA  
CGGTGATTTCTTGGCCGCCGCTGACGGCGCGAACGACGCCAGCGACCACATTAGCANATGGCCAGCGCGTGCCGGGC  
CACGAGGTTGGTGCTCGGCGGCTACTCCAGGGTGCGGCCGTGATCGACATCGTCACCGCCGACCACTGCCCGGCCT  
CGGGTTACGCAGCCGTTGCCGCCCGCAGCGGANNATCACATCGCCGCGATCGCCCTGTTC (SEQ ID NO. 448)

.....Rv343T7.seq:.....  
CCACCCGTGTAATTTGGGATGGGNCNAAAGGCNAAAGCACCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGG  
CTAGGGCTTCTCGCGGAAGGCCGGAACGTACGGCGTTTCAACACGTGCGCTCGCCCTCGACCGCGAACATTGGGG  
ATGGCAGCAACCTGGTAGCACCTTGGCCGGGCGATGATCTGCAGCGTCGCCGCGGGTAGTCGCCGCCGGGCGGCTAC  
AGTCTGAAACGCGATGACCATCGATGTGTGGATGCAGCATCCGACG (SEQ ID NO. 449)



## Clone Rv344

:::Rv344SP6.seq:::

TCAAGCTTTAGCTGCCGAATCCGTANCCCGATGCNCCAGATCGGGGCTTCGCANATAAAGCACNAACAGGCGGGC  
AAAACGTCNATCTCGGAGCCGGAAGGGCAATCANCCGACCGTCNACAAACGACACCGGCGANACCACTTAGGCAGTGA  
CGGCGGCGCCGAACATTACNCGCTCGTTGATTAGGCGTTTCGGTCTCGTCCGCGGTTCATGCCGAGCAGCTTGC CGGCANA  
TCTGAACGCTGTCCTGTCCGGGCAGCGGCGCGGGCGTTGGGGTGCTTGC CGGAATGTGACNAAACGGAGCCGGACCCN  
TCTCGGCG (SEQ ID NO. 450)

:::Rv344T7.seq:::

CCGGGGCCACTCCGCACAATCNGTACNNACCAANATCTACACCATCGAATACGACGGCGTCGCCGANTTTCCGCGGT  
ACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAACCTTTCATCCTGACGC  
CGGAACAAATNGACGCNTCGGTTCCGCTGACCAATACGGTCGGTCCC (SEQ ID NO. 451)

## Clone Rv346

:::Rv346SP6.seq:::

NCTGGCCTTTGGTCCACACTAANACAATACTCAAGCTTCCGGCCGAGAGCCGCCAACTCACGATATCGTTAACCGAT  
ATCCCGAGCCGATAGCTGGCGGGCTCGGGTGGTGGCCAGCGGCGCTGCGACNAAAGGTGTGACCGTCATGAAACAGAC  
ACCACCGCGGCGGCTCGGCCGTCTCACCTGCTCGANATCTCAGCATCCGACGCGGTGTGATCGCGCTTTCCGCGGTG  
TNGTGGGTNCNCCGCCCGAGCCCGGCAAAGGCCGGCCCGACACAACCCCGAAC (SEQ ID NO. 452)

:::Rv346T7.seq:::

CATCTGCCACACACGACCGCGGTGCGGACGCGGCTGACGCGCCTGGTGGTCAGCATCGTGGCCGGTCTGCTGTTG  
TATGCCAGCTTCCCGCCGCGCAACTGCTGGTGGGCGGCGGTGGTTGCGCTCGCATTGCTGGCCTGGGTGCTGACCCAC  
CGCGCGACGACACCGGTGGGTGGGCTAGCGCCTGCTATTCCGGCCTGGTGTCTACGTCTCGTTGTTGCCGTGG  
ATCGGCGAGCTGGTGGGCCCCGGGCCCTGGTTGGCACT (SEQ ID NO. 453)

## Clone Rv347

:::Rv347SP6.seq:::

GACAATACTCAAGCTTGACTGGCCACCCACCGGCATGACCACCGACAGGCCCGACTGGTTCGTACCACTCGAACGCCGG  
GGTGTGATGTCCAGCCGCTGAANTCGTCTGCGCGCGCAGGCCGTCNAACAGGTACAGGGCGGGCGAATTGGCACC  
ACCACTTTGGAATTGGACCTTGATGTACGGCCCATCGACGGCGACGGCACCTGCAGGTACTCCACCGGCAAGCCCCG  
CCGGGAAAATGCCCCCGCGGTNCNCGTGCCACCGACGGCGCCGANCAAAACCGACACTAGGGCCGCGCCNACGGCCCC  
GACCACNANTCNACGCGACATACCCGTGACGGCGCCACNAACCCTGTCAACA (SEQ ID NO. 454)

:::Rv347T7.seq:::

CCTCCAACTCGGCGGGGAAGCGACNCCAGCCTACCGAGCTTGGAGTCCANGACGCCAGCGGCGGCGTGGTCTGCGTC  
GTGGTGCCCGCGGGGTGGCGTTGGCTGGCAACGATCTCCACCCAGCCGGTCGGGTTACCCACGATCTCGGCATANACG  
CGGGCCGAGGCGGCTGCGATACCGTATTGCGTCAATTGGGACGCGGTTGTGCATTCCGGCTAGCTCGGTTGCCACACC  
GTCAGGGGTTTCGACGTTGGCGGGTTCGGCGGGCCCCANACCGCTGTCAACATGCCCGCCAAGCCGACCTGCGGCGCC  
ACCAACTGCAGCACCANCATGTCGCCGTGCGCGCGCCGCGATCACATGG (SEQ ID NO. 455)

## Clone Rv348

:::Rv348SP6.seq:::

CTCAAGCTTTTGTAGCGTCGCGCGGGGCGANCTTCGCCGGCAATTCTACTANCGAGAANTCTGGCCCGATACGGATCTG  
ACCGAANTCGCTGCGGTGCANCCACCCTCATTGGCGATGGCGCCGACNATGGCGCCTGGACCGATCTTGTGCCGCTT  
GCCGACGGCGACGCGGTAGGTGGTCAAGTCCGGTCTACGCTTGGGCCCTTTCGCGACGGTCCCGACGCTGGTCCGCGTT  
GCGCCGCGNAAAGCGGCGGGTCCGATCAGGAATGCCTNCNCCGCCGCGGCACTGCACGGCCAGTGCCGCGGCGA  
(SEQ ID NO. 456)

:::Rv348T7.seq:::

CNCCAGCTTGATTGGTCTGGTTGCATTGGCCAGCTGCGCGAGCCTGGCTCACTTCAACTACGACGACCGCAAACAATT  
GCCGCTTTCGATCCGAGTTCCGTTGGGTACGCGGCAATGGAGCACCATTCTCGGTGAATCAGACTATTCTTGAGTA  
CTTGATCATCCACTCTGCACACGACCTGCGAACCCCGCGCGGCTTGGCGACCTGGAGCAGCTGGCGCAACGTGTGAG  
CCAGATCCAGGCGTTGCCATGGTTCGCGGTGTGACCCGGCCAAACGGGGAAAC (SEQ ID NO. 457)

## Clone Rv349

:::Rv349SP6.seq:::

CAATACTCAAGCTTGACTGGGCCCCGACCTTCGGCGCCACCCACACCGTCAACGCCCGCGAAGTCNACGTCGTCCAGG  
CCATCGGCGGCTCACGGATGGATTTCGGCGGGACGTGGTGATCGACGCCGTGCGCCGACCGGAAACCTACCAGCAGG

CCTTCTACGCCC GCGATCTCGCCGGAACCGTTGTGCTGGTGGGTGTTCCNACGCCCGACATGCGCCTGGACATGCCGC  
TGGTCNACTTCTTCTCTCACGG (SEQ ID NO. 458)

.....Rv349T7.seq:.....  
TCGACGGTTTGGCGGCCTTAAATGCACTGAGGTGCTCAATTGACCCACAGCGGAAATGCCGACTATTTCGACGGCCTC  
CTTCGCCTTGGCTGCCGAGAGGGGCTCCGCGGGAACCGCATGCAGGTATATGACCTCGGTTTCTCGGGTGCTACCGC  
GTGCCTTGTNTANGATNANCTCGGCGTTGGAATTGTCCAGCCGGCCCAATTCATCGAGCGCANATTCTGTACACNTGGC  
CGGCGGCGACATACGCTTCACCGTGGATCTGCTCCACACGGACCGCCCTGTCTGGGATCCTGCTCACGGGTAANGGAAC  
TTACGTGGCACTCGG (SEQ ID NO. 459)

Clone Rv34

.....Rv34SP6.seq:.....  
GACCACGCCAGGCTAATCACGTGACGCTACCGAATACCCTNCTAGTGGTGCAGGCTCCCGCTGGAAATGGCCCTGTA  
CCAACCTCGCGCACCGGTGCCAG (SEQ ID NO. 460)

.....Rv34T7.seq:.....  
CGGCACCCGACCCCTTTGAGCCGTCCGCCGTGGCCGCGGTGGAAGTGGCCGACGAGGGACTGATCGTGCTGGGCAAAT  
TGGTCGATGGCACGCTGGCCGCCGATCTGAAGTCN (SEQ ID NO. 461)

Clone Rv350

.....Rv350SP6.seq:.....  
CTCAAGCTTGCCGTTACCCCGACTTCCGGAGGGACACCATGAGCACCGCCAGCCGAGCACGAGGCCAAACTCCGCCGA  
CGCAGGCCGTTGGACTTGTGCTGCTGGACAAGGGGTTTAGCCCGCGAAGCAGTGACGTACATCGGCGGAAAAGCAGTT  
CGCCTGTGCGACCGACGNGCANNACCGTGAGGCTAGGGAAGCGAGGAGCACATGGCCGCCGACC CGCAATGTACACGCT  
GCAAGCAAACCATCGAACCCGGATGGCTATNCNTACCGCCCATCGCCGCGGT (SEQ ID NO. 462)

.....Rv350T7.seq:.....  
CATGTCGCGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGCGGGATCCCAAAGTGGCGATGATCGGGCCGCC  
TACGTCGTGGTGTAACCTCGTCGTAACAACGAAACCGAAGCGTATGACTCGGTCCACGCGGTGCGGCACATGGTGGAC  
ACCACACCGCCACCGCACGGGGTGAAGGCCATGTGACCCGGTCCGGCAGCACTCAATGCCGACCGAGGCCGAGGCCGA  
GACAAAAGTATCGCTAAGGTCACCGCGATCACGAGCATGGTGATCGCAGCAATG (SEQ ID NO. 463)

Clone Rv351

.....Rv351SP6.seq:.....  
ATACTCAAGCTTCGGTACGGTGGCGGGCCGTGCTGCTGGCCGCGGTGCGGGCGTGGCGGGCTGCGGTCTCGTTTACN  
AGCTCGCGCTGCTGACACTGGCGGCNAGCCTGAACGGCGCGGGATCGTGGCCACCTCCCTGATCGTGGCGGGCTACA  
TAGCCGCGCTGGGAGCAGGCGCCTTGCTGATCAAGCCGCTACTTGACACGCGGCCATCGCGTTTCATCGCCGTGGAGG  
CGGTGCTGGGCATCATCGGCG (SEQ ID NO. 464)

.....Rv351T7.seq:.....  
TGTCAGTCCCTTTCAGATCTNTTTTATGACATGACTGGAGATCTGTCTAGATTGCAGCTCCTGTGAGCGTGGGTAC  
CGGATTCAAGCCGGTGGTACGCCGCGGTGGTACCGGCTTTGCGGCACTGCTCGGCCCTCGAGTTTGGCGATCGCGCG  
CGAAGTGCGTTGCGCGAGCAAGATCGCGGCCGTAATGCCGCGGATGACCGCGATGACCAGCGCGATCCAGGAGAACCG  
TTCCAACCACTGCTGGGCGGCCATCCCGCGAAGTAGACCACTGCACTGGTGCC (SEQ ID NO. 465)

Clone Rv352

.....Rv352SP6.seq:.....  
CAATACTCAAGCTTCAAAACAGGCTGTGTGGGCGCAACCGGCTCGCCGAGTTCTGCACGCACCGCCTCAANTGGCG  
CCCGCACCGCCGGCATCTCCCGTCACGCAGGGCCGCGGCCCGCCGACAGCGNGTGTTCGCGCAGTTTCGCCGT  
CAATGATGCTGACCTGATCGGCCACCGGGCGTTCTCGGCGTCTCNCGTTCACTAATCGCGGTGCTC  
(SEQ ID NO. 466)

.....Rv352T7.seq:.....  
TACGCTGGCGCTGGAGGGAGCCANNTACAACATCCACGCCAATGCTCTTGCCCCGATCGCGGCGACAGGATGACCCA  
GGACATCCTGCCGCCCGAAGTACTGAAAAAGCTCACACCCGAGTTCTGCGCACCGGTGGTGGCCCTACCTGTGCACCGA  
GGAGTGTGCCGACAAACGATCGGTGTACGTGCTGGTGGCAAGGTGCAGCGAGTTGCGCTGTTTGGCAACGACGG  
CGCCAACTTCGACAAACCGCCGTCGGTACAAGATGTTGCGGCGCGGTGGGCGGAGATCACCGATCTGTCCGGTGGCAA  
AATTGCTG (SEQ ID NO. 467)

## Clone Rv353

.....Rv353SP6.seq:.....  
GCTTTTCCCGTCCGTCNNCGCTCAACCGCGTGAGGCCGAAGCGGNTGGTTACGACTCCCTGTTTGTGATGGACCACTT  
CTACCAACTGCCCATGTTGGGGACNCCCGACCGGATGCTGGAGGCCTACACGGCCCTTGGTGCGCTGGCCACGGC  
GACCGANCGGCTGCNNNTGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCCGACCCTGCTGGCAAANATCATCAC  
CACGCTCGACGTGGTTAGCGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGTTGGTTTGANCTGGAACA

(SEQ ID NO. 468)

.....Rv353T7.seq:.....

CNGCTTTTTAATGGCCTTGACNTGGGCGNGCCGGCCACCGGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTAC  
ACCATCGAATACGACGGCGTCGCCGACTTTCGCGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCCGC  
ACCTACTACGTGCACTCCAATACTTTCATCCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTC  
GGTCCCACGATGACCCAGTACTACATCATTTCGCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATC  
GTGGGGAACCCACTGGCGAACCTGGTTCAACCAAATTGAAGGTGATTGTTAACCTGGGCTACGGCGACCCGGCCTAT  
G (SEQ ID NO. 469)

## Clone Rv354

.....Rv354SP6.seq:.....  
CTCAAGCTTGCCGGGAGGGTGCATGGCCGACTCGGATTTACCCACCANGGGGCGCCAACGCGGTGTCCGCGCCGTCNA  
GCTGAACGTTGCTGCCCGCTGGAGAACCTGGCGCTGCTGCGCACCCCTGGTCGGCGCCATCGGCACCTTCGAGGACCT  
GGATTTTCGACGCCGTGGCCGACCTGAGGTTGGCGGTGGACGAGGTGTGCACCCGGTTGATTCGCTCGGCCTTGCCGGA  
TGCCACCCTGCGCCTGGTGGTCGATCCGCGAAAANACGAANTTGTGGTGGAGGCTTCTGCTGCCTGCGACACCCACNA  
CGTGGTGGCACCAGGCTTTAGCTGGCAT (SEQ ID NO. 470)

.....Rv354T7.seq:.....

CCGACGCCGTGCTGGCCACCAACACCGCGACCAGCACCGTGACCCGGACCGGGGTGCCGCGGAACCGGTCTTGCCCA  
ATTGCCGCGGCACCAAGCCGTGCGCGCCATGGCGAACAGCACGCGGCATTGCCCAGCATCAACACCATCACCACCG  
TGTTAAGCCCGGCCAGCGCGCCGACGGAGATGATGCCGCTGGCCAGTACACCCCGTTGGCCTGGAACGCGGTGGCCA  
GATTTGCCGGCCCGCGGCCCGGTACGGTCCGCAGTTGGGTGTATGGAACCATGCCCGACACCAACCG

(SEQ ID NO. 471)

## Clone Rv355

.....Rv355SP6.seq:.....  
TTNACTGGCCTTTGGTCCACACTAGACAATACTCAAGCTTCCAGGACATCGTCATCGCGACCAAAACCGCGAGCTAGG  
TCGGCATCCGGAAGCATCGCGACACCGTGGCGCCGAGCGCCGCTGCCGGCAGGCCGATTAGCGGGCAAATTAGCCC  
GCCGCGGCTCCCGGCTCCGANTACGGCGCCCCGAATGGCGTCACCGGCTGGTAACCACGCTTGCAGCGCTGGGCGGCG  
GCCTGCCGGATCAGGTGGTAAATGCCGACA (SEQ ID NO. 472)

.....Rv355T7.seq:.....

NGACGTCTTCCATCCGCGCTGTTTTGGCGGGTTGGCCACAGCAGCCCGCGGTGACGGCGACGATGCTGGGCTGGT  
TGCGGCCCTGCGCCACCGCGCTTGCATGCTGGTTGGCTGTCTTGGGACGATCCCGAAATAGTCCACGCGGATCTGGT  
GATTTTGCGGGCTACCCGCGATTACCCCGCGCGGCTCGACGAGTTTTTGGCCTGGACTACCCGCGTGGCCAATCTGCT  
GAACTCGCGGCCGCTGGTGGCCTGGAATGTCGAGCGCGTTACCTA (SEQ ID NO. 473)

## Clone Rv356

.....Rv356SP6.seq:.....  
CTTCCTCCTGAGTACCNCCGNTACTTTGGGATGGGTAAGGCGAATCNCCTTTGGTTCAGAACGCCGGGAGGG  
ACAATCTCGGGCGGCTGGGGCCTCTCGCGGAANGCCCGAATGTACGGTGTCTCGACACTTCCNTCCCCCTCCG  
(SEQ ID NO. 474)

.....Rv356T7.seq:.....

GAGCATCGGGACNTACGGAGTCAACTACCCGGCCAACGGTGATTTCTTGGCCGCGCTGACGGCGCGAACGACGCCNG  
CGACCACATTGAGCAGATGGCCAGCGCGTGCCGGGCCACGAGGTTGGTGCTCGGCGGCTACTCCAGGGTGCGGCCNT  
GATCNACATCGTCACCGCGCACTGCCCCGCCCTCGGGTTCACGCAGCCGTTGCCGCCNCAGCGGACGATCACNT  
CGCCGCGATCGCC (SEQ ID NO. 475)

## Clone Rv357

.....Rv357SP6.seq:.....  
TACTCATGANCATCCTTTAATCANNGCTTTGCGTTTTTTTATTAAATCTTGCAATTTACTGCAAAGCAACAACAAAT  
CGCAAAGTCATCAAAAACCGCAAAGTTGTTTAAATAAGAGCANCACTACAAAAGGAGATAAGAAGAGCACATACCT

CAGTCACTTATTATCACTAGCGCTCGCCGAGCCGTGTAACCGAGCATAGCGAGCGAACTGGCGAGGAAGCAAAGAAG  
AACTGTTCTGTGATAGCTCTTACGCNCA (SEQ ID NO. 476)

Clone Rv358

.....Rv358SP6.seq.....  
CTCAAGCTTCAGGTCAATGTGCNCCAAGCCCTGACGCTGGCCGACCAGGCCACCGCCCGGANACNCTGCCAAGGCC  
ACCGAATACAACAACGCCCGGAGGCGTTTCGCANCCAGCTGGTGACCGCCGAGCANANCGTCAAAAACCTCAAGACG  
CTGCATGACCAGGCGCTTANCNCCGCANCTCAGGCCAAGAAGGCCGTNAACGAAATGCGATGGTGCTGCACCANAAG  
ATCGCCGAGCGAACAAGCTGCTCAGCCNG (SEQ ID NO. 477)

.....Rv358T7.seq.....  
CATGGTGGCACTGTAGCGACGTGCTGCAATCAAGGTGATGCCCCACTCTGGTCAGCTCGGANCCGCTGACACCCCGCT  
AAGGCTGCTCAGCTCGGTGCATTACCTACCGACGGCGAACTCCCCAGCTTTACGACTATCCGGATGACGGCACCTG  
GTTGCGGGCGAACTTCATCATCAGCTTGACCGGCGGCGCTACCGTCGATGGCACCAGCGGGGCGATGGCCGGGCCCCG  
CGACCGATTCTGTTCAACCTGTTGCGTGAAGTTGCCGACGTCATCGTGGTGGCGGTGGGCACCGTGCGCATTGAGGG  
CTACTCCGGCGTCCGGATGGGTGTCGTCCAGCGCCAGCAC (SEQ ID NO. 478)

Clone Rv359

.....Rv359SP6.seq.....  
TACTCAAGCTTGCGGGTGATCGCCTTGCTCAACGGCACCCTGATCGGATCGGGGTCNACCGCACAAATGGACTGGAGC  
TTCGGCGAANTCATCGCCTATGCCTCGCGGGGGGTGACGCTGACCCCGGGTGACNTGTTCCGGCTCGGGCACGGTGCCC  
ACCTGCACGCTCGTCTATCACCTCNGGCCACCGGAATCATTCCCAGGCTGG (SEQ ID NO. 479)

.....Rv359T7.seq.....  
GTTGGNGCCTCGTCGGCGAACAGTTCTCGCACGATTTCCGGATTAGCGGGACTGGTCACCAGTTGGGTATGCGGGAAG  
GCGCTGACGTTCCGCCGCTTAGCTGTTTGATGGACGCGGTGGTGATGTTCTGATCACGGAAGTGGCTGTAATAGCCC  
AGGGTCGCCACGCTTTCATCCGGGCCCCGACCCGGCGCACCGAGCGTGTCGCGCAGGTATGCGACGTGATTTTCGCTG  
AAGTCCCCGTACCCGGAGAACT (SEQ ID NO. 480)

Clone Rv35

.....Rv35SP6.seq.....  
TGCTTCCGGCTCGTATGTTGTGTGGAATTGTGANCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG  
CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTCCAGGTCAATGTGCGCCAAGCCCTGACGCTGGCCGACCAGG  
CCACCGCCGCGGAGACGCTGCCTTTGTACCGAATAACAACGCCCGGAGGCGTTTCGACGCCAGCTGGTGACCG  
CCGAGCAGAGCGTCGAAGACCTCAAGACGCTGCATGACCAGGCGCTTAGCGCCGACGCTCAGGCCAAGAATGCCGTCG  
AACGAAATGCGATGGTGCTCGGCATAAGATCGCCGAGCGAACAAGCTGCTCAGCCAGCTCGAGCAGGCCAAGATGC  
ACGAGCA (SEQ ID NO. 481)

.....Rv35T7.seq.....  
CAGGCATGCAAGCTTCGGAGGCAGACCCGTGCATGGTGGCACTGTAGCGACGTGCTGCAATCAAGGTGATGCCCCACT  
CTGGTCAGCTCGGAGCCGCTGACACCCCGCTAAGGCTGCTCAGCTCGGTGCATTACCTACCGACGGCGAACTCCCC  
AGCTTTACGACTATCCGGATGACGGCACCTGGTTGCGGGCGAACTTCATCAGCAGCTTGGACGGCGGCGCTACCGTCG  
ATGGCACCAGCGGGGCGATGGCCGGGCCCCGGCAGCCGATTCGTCTTCAACCTGTTGCGTGAAGTTGCCGACGTCATCG  
TGGTCGGCGTGGGCACCGTGCGCATTGAAGGCTACTCCGGCGTCCGGATGGGTGTCGTCCATCGCCA  
(SEQ ID NO. 482)

Clone Rv360

.....Rv360SP6.seq.....  
TACTCAAGCTTGGGGTGGCGCTGTCCGGTCGGTGTGCTTGGCGGCGTCGGTATCAACACCGCCACGAAATGGGGCACA  
AGAAGGATTGCTGGAGCGGTGGCTGTCAAATACCCCTCGCCCANACCTGCTACGGGCACTTCTACATCGAGCACA  
ACCGTGGCCATCAGTCCGGGTGTCCACACCGGAGGACCCGGCGTCGGCGCGGTTCCGGCNAACGTTGTGGGANTTCC  
TGCCCCGCANTGTTATCGGCGGCTTGCGCT (SEQ ID NO. 483)

.....Rv360T7.seq.....  
GGCCATCGCCACCGCNCCGCGGCGAACGCTCAAAGGCACCTACTGGCACCAAGGCCCCACACGTCACCCCTGTGACCTC  
CTGCGCCGACCCCGCCGAGGTCCTGGCCGTTACCACCGAACGGGCGAGCCGGGAGTCTGGTACGCATCGAACAAGA  
GCAAGGTGCATGGGCGGAGTTGTTCCGCCACTTCGTCGATGACGGGGTCGATCCATTTCGAGGTCCGTCGCCGCGTCGG  
TCGAGTGGCGGTCACACTCCANGTACTCGACCTCACAGACGAGGAGTTCGATCCCATCTAGGTGTGGACGAAACAGA  
TCTTCTGTCCGACGACTACACCACCCAGGCCATCGC (SEQ ID NO. 484)

## Clone Rv361

.....Rv361SP6.seq.....  
GCTTGCGGGTGATCGCCTTGGTCAACGGCACCGTGATCGGATCGGGGTCNACCGCNCAGATGGACTGGANCTTCGGCG  
AANTCNTCGCCTATGCCTCGCGGGGGGTGACCCTGACCCCGGGTGACNTGTTGCGCTCGGGCACGGTGCCACCTGCA  
CGCTCGTCAAGCACCTCNGGCCACCGGAATCATTCCCGGGCTGGCTGCACNACGGCGACNTGGTCNCCCTCCAGGTCCG  
AAGGGCTGGGCNAAACAANGCAGACCGTCCGGACAANCGGCACTCCTTTTCCGTTGGCTCTTCGGCCGAATCCGGACG  
CCNAACCCGACCGGCG (SEQ ID NO. 485)

.....Rv361T7.seq.....  
GTTCTCGCACGATTTCGGATTAGCGGGACTGGTCACCACTTGGGTATGCGGGAAGGCGCTGACGTTCCGCCGCGATTA  
GCTGTTTGATGGACGCGGTGGTGATGTNCTGATCAGGAACTGGCTGTAATANCCAGGGTCGCCNCGCTTTCATCCG  
GGCCCGGACCGCGCACCGAGCGTGTGCGCGAGGTATGCGACGTGATTTTCGCTGAAGTCCCGTACCCGGAGAAT  
CGAACACGCTGAGGCGCTCGTCACCGTCTGNNCGGCGACCAAGCGCGGCGAGCAACTGCGCAAAATCGTTAAGANAGG  
TCGAATCGTTGAAATTCGGCACCACTGCACC (SEQ ID NO. 486)

## Clone Rv363

.....Rv363SP6.seq.....  
CACAAGACAATACTCAAGCTTCAGGTCAATGTGNCNCAAGCCCTGACGCTGGCCGACCAGGCCACCGCCCGCGGANAC  
GCTGCCAAGGCCACCGAATACAACAACGCCGCCGAGGCGTTTCGACGCCAGCTGGTGACCGCCGAGCANANCGTCNAA  
AACCTCAAGACGCTGCATGACCAGGCGCTTANCGCCNACGCTCAGGCCAAGAAGGCGCTCGAACGAAATGCGATGGTG  
CTGCAGCANANATCGCCGANCGAACCAAGCTGTCAGCCAGCTCGAGCAG (SEQ ID NO. 487)

.....Rv363T7.seq.....  
CCACCCGTCATGGTGGCACTGTAGCGACGTGCTGCAATCAAGGTGATGCCCCGACTCTGGTCAGCTCGGAGCCGCTGA  
CACCCCGCTAAGGCTGCTCAGCTCGGTGCATTACCTCACCAGCGGCGAACTCCCCAGCTTTACGACTATCCGGATGA  
CGGCACCTGGTTGCGGGCGAACTTCATCAGCAGCTTGGACGGCGGCGCTACCGTCGATGGCACCAGCGGGGCGATGGC  
CGGGCCCGGCGACCGATTCTGCTTCAACCTGTTGCGTGAACCTTGCC (SEQ ID NO. 488)

## Clone Rv364

.....Rv364SP6.seq.....  
GCTTTCCGCCGATACCCNCCATGTCCCGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGCGGGATCCCAAAG  
TGCGGATGATCGGGCCGCTACGTCTGTTGTACCTCGNCGGTAACAACGAAACCGAANCCTATGACTCNGTCCACGC  
GGTG (SEQ ID NO. 489)

.....Rv364T7.seq.....  
CAACCCGANTTGGCTTTCGGCGCCNTCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCGTCCGCGGGACACAC  
CTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGATCTACNACGCCGNGNGGAACGCTTCNGCCGC  
GGGCGTGACCGCNTCCCGTT (SEQ ID NO. 490)

## Clone Rv365

.....Rv365SP6.seq.....  
GGGATGGGCAAAAAGGCGAAGCACCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGGCTAGGGCTTCTCGCG  
GGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGTTCGCCCTCCGACCGCGAACATTGCGGGATGGCAGCAACCTGG  
TAGCACCTGGCCGGGCGATGATCTGCCAGCGTCCCGCGGGTAGTCGCCGCCCGGGCGG (SEQ ID NO. 491)

.....Rv365T7.seq.....  
CAGCAGACCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGGCCAACGGTGATTTCTTGCGCGCGCTGACGGC  
GCGAACGACGCCAGCGACCATTCAGCAGATGGCCAGCGCTGCCGGGCCACGAGGTTGGTGCTCGGCGGCTACTCC  
CACGGTT (SEQ ID NO. 492)

## Clone Rv366

.....Rv366SP6.seq.....  
CTCAAGCTTGACTGGCCACCCACCGGCATGACCACCGACAGGCCCGACTGGTTCGTACCACTCGAACGCCGGGTGTTT  
GA (SEQ ID NO. 493)

.....Rv366T7.seq.....  
TTGGTGCCCGAATGGCGAGTCCCATTTANTCGCTGATTTGTTTGAACAGCGACGAAACCGGTGTTGAAAATGTCGCC  
TGGGTGCGGGATTCCCTCTCCAAGCAAGAGTAACTGGCCCCAAATAAAGTTACTCGTCTTGCAAAGACCGCTACC

CGATGCCATTTATGTGTTTCCTTACGCTCNNNNTTCCGGTGCGCCATCATTATCTGCACCTTTGCACTGCACATTGAG  
CTTAGCAGCGCTCG (SEQ ID NO. 494)

## Clone Rv367

.....Rv367T7.seq:.....  
GAATTNGCTTTTCGGCGCCATCGGCCCAGGACCGCGTGCGGGTGCTCAACGACGACGTCGTCCGCGGGACACACCTCGA  
TGCTGCCGCCATGGACGCGGTGGAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCCGCGCGGGCG  
TGACCGCATCCCGTTGACCGGGCGGATCGCNGTGATCGTCGATGACGGCATCGCCACCGGAGCGACGGCCAAAGGCGGC  
GTGCCAGGTGCGCCGGGCGCACGGTGCGGACAAGGTGGTGCTGGCGGTCCCGATCGGCCCAGACGACATCGTGCGGAG  
ATTCGCCGGGTACGCCGATGAAGTGGTGT (SEQ ID NO. 495)

## Clone Rv368

.....Rv368SP6.seq:.....  
TAAAGCTTTTCGTAGTTCATNGNGCCCCGGACCAACAAAAGCATCGGGACATACGGAGTCAACTACCCGGCCAACGG  
TGATTTCTTGGCGCGCTGACGGCGCNAACGACGCCAGCGACCACATTGAGCAGATGGCCAGCGCGTGCCGGGCCAC  
GAGGTTGGTGCTCGGCGGCTACTCCAGGGTGCGGCCGTGATCNACATCGTCACCGCCGACCACTGCCCGGCCCTCGG  
GTTACGCGAGCCGTTGCCGCCCCGAGCGGACGATCAANTCGCCGCGATCGCCCTGTTGCGGAATCCCTCGGGCCGCGC  
TGGCGGGCTGATGAGCGCCCTGACCCCTCAATTGCGGTCCAAANACCATCNACCTCTGCAACAACGGCGACCCGATTTG  
TTCGGACGGCAACCGGTGGCGANCGACCT (SEQ ID NO. 496)

.....Rv368T7.seq:.....  
CCGGGAGGGACCATCNCGGCGGCTNCGGCTTCTCTCCGGAAGGTTCTANNGTNNNGCGTTTCNACNCTTCCCGTCGC  
CCTGCGACCGCCGAACATTGCGGGTATGGNNGCANCTGTNAGCATCCNGGCCGGG (SEQ ID NO. 497)

## Clone Rv369

.....Rv369SP6.seq:.....  
CTCAAGCTTCCGCATCAGATCGCTATAGAACCAGGTGCGCGTCCCCACCGAGTGGCTGGTGCCTTCCAGCACGATCGT  
TACCGCGTTATCGGAATCAAACCTNCCGAACACCTGACCAACGCGCTTGATCGCCTGAATCGATGCGGCGTCGCTGGG  
GCTCATCGATACCGAGTGTGCTTTCCGACCACTTCCAGTTGCGGTACGGCGAGATTGACAAAGGCGGTGAAGCCCCAG  
CCAGAGCAGGACGATCACCNCCGAAACCGGCGGATTGCCCC (SEQ ID NO. 498)

.....Rv369T7.seq:.....  
GCTTGGCAGCCTGCGGCTGGGCGCCCTNGAGCTCTTCGATCTGGATCTCCGGACTCGAGATGCTCACTTGCCCCGGCCG  
TGGACGTACCCATTGCGGCCGGGACCCAGCGCCCCAGGTGACCAGCGAGTTGGGCTGCACGCTGACCCGGCCGTCGG  
GGTCGACGCCGGTAACGGTCAGCAGCTCCGANGTCCNNTGATCCCGACCGCAGCTGCCAATGCGCGGTGGCAGCCG  
ACGTGGATGTGCCGGGGCCCTAGATCGCGGGGACGAGACCGCGTCACCGACGGTCATCACCTTGCCGAGTTTNG  
GCCTGCCGCAN (SEQ ID NO. 499)

## Clone Rv36

.....Rv36SP6.seq:.....  
GCTTCCGGCTCGTATGTTGTGGAATTGTGAGCGGATAACAATTNCACACAGGAAACAGCTATGACCATGATTACGC  
CAAGCTATCTAGGTGACACTATAGAATACTCAAGCTTGAGCCATCGGGCTATCAGCTGGTTGATGTCCCG  
(SEQ ID NO. 500)

.....Rv36T7.seq:.....  
CAGGCATGCAAGCTTGTGCTCTATCACATCCGACCACCAACCGCCGACGGCTCGGCAGAACGCCTCCGCATATGGGT  
CGACGACCGCGGGTTCGGACTTCTGGGCTGCCAGCGCTCGCGCCGTGCGGACAAACAGCGCGGTGCAACCGACACTCC  
TTGTGATGTCCACCTATCACCTTCGGTACGCACCCAATCGACCTACGCGGTAGCTCAGCCCCGATCTTCCAGAGC  
TCCGCCCC (SEQ ID NO. 501)

## Clone Rv370

.....Rv370SP6.seq:.....  
GCTTTTTCGAGCGTCGCGCGGGGCGGCTTCCCCGGCAATTCTACTAGCGAGAAGTCTGGCCCCGATACGGATCTGACCGA  
AGTCGCTGCGGTGACGCCACCCCTCATTGGCGATGGCGCCGACNATGGCGCCTGGACCGATCTTGTGCCGCTTGCCGA  
CGCGACGCGGTAGGTGGTCAATTCCGGTCTACGCTTGGGCTTTCGGGACGGTCCCGACGCTGGTGCAGGTTG  
(SEQ ID NO. 502)

.....Rv370T7.seq:.....  
CGANCCTGTTTCGACGGCTACCTGAATCACCCCGATNCCACCGCCGCGGCGTTTCGACGCCGACAGCTGGTACCGCACCG  
GCGACGTCGCGGTGGTTCGACGGCAGTGGGATGCACCGCATCGTGGGACGCGAGTCGGTCGACTTGATCAAGTCGGGTG  
GATACCGGGTCGGCGCCGGTGAAATTGAAACGGTGCTGCTCGGCCATCCGGACGTGGCGGAGGCGGCAGTCGTCGGGG  
T (SEQ ID NO. 503)

Clone Rv371  
.....Rv371SP6.seq:.....  
NAAGCTTTGTACACCAAGTGTTCNACCAGNCGTCCATCCGGCGAAGTGGATACTCCAGCAGGTAGCAGGTGCGC  
ACCACGCTGGTCAGTCGCGCTTCAGCTCGCTTGCGGCGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTGGCG  
(SEQ ID NO. 504)

.....Rv371T7.seq:.....  
CGCTGGNCGCCGGCGCTGGGCTGCGGTAAACCAATTACCACAACACTTTTCGGTAGCCGAACAGCGGCGCTACCAGCG  
AAATGGCACAGCCACCGCAGTCGCGGACATCCCGGAAGATGTGGCAGATTTTCGTGCGGTTCGAGCCGGCGAAGGCCT  
AGCGTCATTGTTGCGCTGGCAAGGTTGCTGGGCCCGG (SEQ ID NO. 505)

Clone Rv373  
.....Rv373SP6.seq:.....  
CTCAAGCTTCTTCTGCCCCCTTGCCGTTNCGGATNACATCCCGCAGCGACTCGGCTTCGGCGTCGATGTCGAAGTTCTC  
GATCAGCTTCTGGATCGACTCCGCGCCCATGGCACCGGTGAAGTACTCGCCGTAGCGGTTCGACNAGTTTCGCGGTAGAG  
GTTTTCTGTCNACNATCAGCTGCTTGCGGCGCCANCTTGGTGAAAGTGCTCCAAATGTCCTCCAACCGGTCCAGCTCACG  
CTGCGCGCGGTACGGATCTGGCGCATCTCGCGCTCGCCGCGTTCGCGAACTTGCGCCGCGCATCGGCCTTGGGGCCC  
(SEQ ID NO. 506)

.....Rv373T7.seq:.....  
GTTACACCTACCTACTATGCCNCAATTCNCCGACACGGGTGGCATCAACACGGGCGATAAGGTGGAAATCGCTGGGG  
TGAACGTCGGGCTGGTGCCTCGCTGGCAATCCGCGGCAACCGCGTGTGATCGGATTCTCGTTGCCCGGCAAGACAA  
TCGGGATGCAAAGCCGGGCGAGCAATTCNCCNACACCATTTTGCCCGTAAGAACCTGGAGATCGAACCCTCGCGGT  
CGGAGCCGTTGAAACCCAACGGTTTCTGCGCTTGCGCGCANACCACTACGCCATACCAAATC (SEQ ID NO. 507)

Clone Rv374  
.....Rv374SP6.seq:.....  
CTCAAGCTTTACGCCGACGCCGGCTACACAACACCAAGGAAACGATTGCCTACTGCCGAATCGGGGAACGGTCCTCG  
CACACCTGGTTCTGTGTCGGGAATTACTCGGACACCAAACGTCAAGAACTACGACGGCAGTTGGACAGAATACGGC  
TCCCTGGTGGGCGCCCCGATCGAGTTGGGAAGCTGATATGTGCTCTGGACCC (SEQ ID NO. 508)

.....Rv374T7.seq:.....  
TCCNCATGGGATAACGGGTTTAGATTTNACAACGGCACCGTGTTTCTCAACAAGCCGGTCATCAGCTGGGCGGCG  
ACAACGGTATCTACTTCACCGCTTTGCGCCGTACAAGAAAACCACTAGGCCACCATCGAGTCCAAGAACAACCAAC  
TGGTCCGCAAGTACGCGTTCTACTACCGCTATGACACCGCCGAGGAACGCGCCGTGCTCAACCGGATGTGGAAGCTGG  
TCAACGACCGCCTCACTACCTCACCCCGACCATCAACCGATC (SEQ ID NO. 509)

Clone Rv375  
.....Rv375SP6.seq:.....  
CTCAAGCTTGGGTGTGCGGATCACCGGAAGCCNATGATCAGCCACGTTTCGCGCCGCCCGGCATACGGCGGCGTAC  
CGATCTCCGCGTCATACACCCGCGGGTAATCGCCGACGGTGCCGTTTCGCGAGCCGAAGGTGACAACGCTGATTGAAT  
CNAGTTCCANGTCCAGCGGGT (SEQ ID NO. 510)

.....Rv375T7.seq:.....  
TNAACAGCTCGCGGCAGCCACGACCTGCTGCGTCGGATTGCGGCGGCGAGATCAATTCCAGGCAGCTCCCGGACAA  
TGGGCTCTGCTGGCCCGCAACGAANGACTCGAGGTACCCCGGTGCCCGGGGTGCTGGTGCACCTGCCGATCGCACA  
GGTTGGCCCAACCGGCGGCTTGTGNNNNGTGCGCAAGCCCGGAGTNGCCAAACCCAGCGTGATCANGCTCGGCT  
CGCGAGTTGCGGCAANAAGTGGCTCGCCTGATCACCTACCATCGGCCANGATCTGCGTGTCA (SEQ ID NO. 511)

## Clone Rv376

.....Rv376SP6.seq:.....  
GCCANCCGGCTTGGCGTCGACTCCCGTTCNGCACATCATACGGTCCCCGGTACTGTCCAACGCGCCGGTGCGCTAGC  
CAAACGTCACGACTCTCAGTGATCCAGTTCGTGATCCGGCCGGTGGCGCCGCTGCGGCGGGGGCTNATNTACTTTCGG  
ACTNATTATCTCATCCAAAGGACACCGGGCCGGTGGCTGGAATCCCATGGTGCGATCGGCCACACAN

(SEQ ID NO. 512)

.....Rv376T7.seq:.....  
CCGACCTGGTATCTTCCGATAGCGCGCTTGATATCCGGTCTGATCTCCTGCCCTTAACGCCGGATCTCAGCAGGTCC  
CCATGCAAAGATCCGAGGTGTCCNGATCTAGGGGTCTCTGCTCCTCCAGATGATGGAGCAAGTCGGCCC

(SEQ ID NO. 513)

## Clone Rv377

.....Rv377SP6.seq:.....  
CTCAAGCTTCGGCTCAGGCGGCGCTGCCGGTAACGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTCGGG  
GGCTACGTGCCATCAAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTACAAACAAATCGCGGTATGC

(SEQ ID NO. 514)

.....Rv377T7.seq:.....  
CATCACCTGHTTCATGAACGGAAGCACCGCAGCGCTTCCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCGGCGGT  
CGGGTGAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAACCAGCTTCCATATCCCGCGACGAACGA  
CGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGGTTCTCCACCGACCGGGCCGGGTGTGGG  
GTGT (SEQ ID NO. 515)

## Clone Rv378

.....Rv378SP6.seq:.....  
AGCTTAGCTTCCCGCCCGCAATAGGGCTCCAGCTCATCCGGTGTGACCAGATAGGGGGCCAGGGTGATACCGCTGT  
CTTTGCCCTTGGCCTGTCCGATGCGCAGCTGGCCCTCCAGCATCTGCAGTCCCGTGCGGACCAGTCGTTGAAATGG  
TATAGCCGATGATCGACCG (SEQ ID NO. 516)

.....Rv378T7.seq:.....  
CCNGAACAGAAGCGGNGGTTCTTACCGCGGTGTGCGGCCGGCGCGATATCGGCCTTTTTACTAACCAGAACCCGATGTG  
GGCTCCGATCCGGCGCGCATGGCATCGACGGCGACGCCGATCGATGACCGCCAGGCTTACCACCTT

(SEQ ID NO. 517)

## Clone Rv379

.....Rv379SP6.seq:.....  
CTCAAGCTTGCGCGACTCGACAAGCATCTTGACAGTTGTTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCCA  
CCAGATCATCTGGTCCGGTAGCGCTCGTCCGGGTATGCTGCCGCCGGGATTCTCGCTGCTATTACTCCCCCGAAGA  
ACGCCACCGGTCCAGCGC (SEQ ID NO. 518)

.....Rv379T7.seq:.....  
GCNAGGCGGTATAGCTTCCCGTCGTACCGCGACCGCCAGCCGAGAAAGCTCGTTTTCCAGTGTTGCTGGGGATTCTC  
ACGCTGCTGCTGAGTGCGTGCCAGACCGCTTCCGCTTCGGGTACAACGAGCCGCGGGGCTACGATCGTGCGACGCTG  
AAGTTGGTGTCTCCATGGACTTGGGGATGT (SEQ ID NO. 519)

## Clone Rv37

.....Rv37SP6.seq:.....  
GTGTGGAACCGTGAGCGGATAACAATTTACACAGGAAACAGCTNTGACCTTGATTACGCCAAGCTATTTAGGTGAGG  
CTATATTAATACTCAAGATTGCGGTCGAGCACATCGGCCCAAGAACCGCCGAAGGCACGGCGGAACGCCTGCGGCACA  
TGGGGCGACGACCGAGCGGGTCCGACTTCTGGGCTGTCCAGCCGGATCGCGCCGTGCGGA (SEQ ID NO. 520)

.....Rv37T7.seq:.....  
CACTGTCAGTACATATGCGCCGCTCCTCCTCATCGCTCGGCATCGTCGCCGGCGGTTCATGGCGTCACCCTACC  
CAAGCCGAACGCGAAACGAGAAGTGTTCATTATTAGGGTGTGAGCACCAATACCAGATTGCTCACCAGGAACTCAC  
GCAGCACCGGGACGGATGTCAGCCACCACGCCATCTGGGGTGGTAGCGGGGAAATACGGCTAACGCGGCTCCGGTGC  
CGGCAGCCAGCGCAGACCCTCGGCCGGCGGACACGGCAAACAACGACGACCCATAGTTGTTCTTTGCCGGATGGCCGT  
GTTTGCGGACATATCGGGCGGGCGGCGGGCGCCGCGAGGTAGTGCTGAGGCCATCTCGTCCCCGCCGAATGGCC  
CCAGCCAAACCGTGTA (SEQ ID NO. 521)



## Clone Rv381

.....Rv381SP6.seq:.....  
CTCAAGCTTTTACGGTGATCGCGCATCACCTGGTTCATGAAGTGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCAACA  
TGAGCCANCCTCTCGTCGGCGGTGCGGTGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCTGAAACCAG  
CTTCCATATCCGCGACNAACGAC

(SEQ ID NO. 522)

.....Rv381T7.seq:.....  
CTCAGAAGCCGCTAGCTGGTAGAGTCGCTGACCGGTGCACGTGGCGNCAATGTGCGCTGCCGGTTCGCG

(SEQ ID NO. 523)

## Clone Rv382

.....Rv382SP6.seq:.....  
CTCAAGCTTGCGCTCATCAAGCGCAACAGCAGGGCGGTGCGGTGGTGCCTCATGACGGGTGACGGGACCAATGACGCA  
CCGCGCTCGCGCAAGCCGATGTCGGGGTGGCNATNAATACCGGCACCCAGGCGGCGCCGGAAGCCGGCAACATGGTC  
NATCTCCACTCC

(SEQ ID NO. 524)

.....Rv382T7.seq:.....  
ACTTCTATTTGACTGGTGTGCTGTGGCGCGATCCGACTGCCGGCGTGGTCAAGGCCGGCCAGTTGTGGGATNCCACA  
GGCAC

(SEQ ID NO. 525)

## Clone Rv383

.....Rv383SP6.seq:.....  
GCTTGTGCTATTCCGTGGCACTGTCAGACATATGCGCCGCTCCTCCTCATCGCTGCGCTCGGCATCGTCGCCGGCGGT  
CATGGCGTCACCCTACCCAGCCGAACGCGAAACGAGAAGTGTTCATTATTAGGGTGTGAGCACCATAACAGATT  
GCTCACCAGGAACCTAC

(SEQ ID NO. 526)

.....Rv383T7.seq:.....  
CGATATTCGTCGGCCGCGTTGTCTCGACTGGGTGCGGT

(SEQ ID NO. 527)

## Clone Rv384

.....Rv384SP6.seq:.....  
GACCTCGGCCACCAAGCCGGACGCGACCGTCGAGGTGGCGATCCGGCTTGGCGTCGACCCGCGTAAGGCAGACCACAT  
GGTCCGCGGCACGGCCANCTGCCACACGGCACTGGTAAGACTGCCCGCGTCGCGGCN

(SEQ ID NO. 528)

.....Rv384T7.seq:.....  
CCGGAAGTCTAGGGGACGACCTACTCAGCGCAAAATGTCGCTAATGTGAGTCCGCCCCACCAGGGCAGATCAACCCAT  
GTGATGATGACCTACCCGGATACCGGATTGGCGGT

(SEQ ID NO. 529)

## Clone Rv385

.....Rv385SP6.seq:.....  
AGCTTCAGTTCCTCCACGACGCGTCCCAAATGAATTTCCGATCCCAATCTCGGTTAGATACAGGTGCCATAC  
CCCTTACTTCGNAACGCTGGGCGGATTGGCCCTGCCGCTG

(SEQ ID NO. 530)

.....Rv385T7.seq:.....  
CCGCTACGGGTGCAACATGCATCCGAGACCGATGCTCGAGCGCGCACCCCACTCGCCGATGGCCGGAACCGGTGG  
TTACCCGGGTGGCGGCTGACC

(SEQ ID NO. 531)

## Clone Rv386

.....Rv386SP6.seq:.....  
GCGGCTGGTTACGACTCCCTGTTGTGATGGACACTTCTACCAACTGCCCATGTTGGGGACGCCCCGACCAGCCGATG  
CTGGAGGCTTACACGGCCCTTGGTGCCTGGCCACGGCGACCGAGCGGCTGCAACTGGGCGCNTTGGTNACCGGCAAT  
ACCTACCGCAGCCCGACCTGCTGGCAAAGATCATCACCACGCTCGACGTGGTTAGCGCCGGTTCGAGCGATCCTCGGC  
ATTGGAGCCGGTGGTTTGGCTGGAACACCGCCAGCTCGGCTTCGAGTTCGGCACTTTCAGTGACCGGTTTCAN

(SEQ ID NO. 532)

.....Rv386T7.seq:.....  
GCCTTTCCGCACAATCTGTACCCAGGACCNTCTAAAAAATCGAATACGACGGCGTGGCCGACTTTCCGCGGTACCCG  
CTCAACTTTGTGTCGACCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTTCATCCTGACGCCGGA  
CAAATTGACGCAGCGGTTCCGCTGACCANTNNTGTCGGTCCCACGATGACCCAGTACTACATCATTTCGCACGGAGAAC

CTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAACCAAACCTTGAAG  
GTGATTGTAACTGG (SEQ ID NO. 533)

Clone Rv387

.....Rv387T7.seq:.....  
GCAGACCAACAAGATGCATCGGGATCATACGCCGTCAACTACCCGGCCAACGGTGATTCTTGGCCGCCGCCAC  
(SEQ ID NO. 534)

Clone Rv388

.....Rv388SP6.seq:.....  
CTCAAGCTTGCCAAAGAGACCTCGTCCACCAAGCNGGACGCGACCGTCNAGGTGGCGATCCGGCTTGGCGTCCACCCG  
CGTAAGGCANACCANATGGTTCGCGGCACGGTCAACCTGCCACACGGCACTGGTAANACTGCCCCGCTCGCGGTATTC  
GCGGTTGGTGAAAAGGCCGATGCTGCCGTTGCCGCGGGGCGGATGTTGTCGGGAGTGACAATCTGATCGANAGGATT  
CAGGGCGGCTGGCTGGAATTCGATGCCGCGATCGCGACACCGGATCAGATGGCCAAAGTCGGTCNCATCGCTCGGGTG  
CTGGGTC (SEQ ID NO. 535)

.....Rv388T7.seq:.....  
CCACGGCGTGGATCAAGGTACCGCGCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTCGGCGTTAGCGC  
CGGATTCCACCACATCCCCCTTGCAGAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCCATCGAGATAGTGGAGCA  
ACGCAATCCGTGCGGTACGGTTCGGGTCNTACTCGATGTGCGCGACCTTGGCGTTGACACCATCTTGTTCATTGCGGC  
GAAAGTCGATCATCCGGTAAGCGCGCTTATGACCGCGCCTTTGTGCCGGGTGGTAATCCGGCCATGCGCGTTGCGTC  
(SEQ ID NO. 536)

Clone Rv389

.....Rv389SP6.seq:.....  
GGCGGCTGCGTCGGCGAGATGATCGCCCGGTGCCACCCGATCCGTGCCTCGGTGAGCGCCAACGTGCTTCCGGTCC  
GGCGACCACCATGTCGCATGCGCCGAC (SEQ ID NO. 537)

.....Rv389T7.seq:.....  
GCAATCGCCTTGGCGGTGCGCGGTTGTACCGGTGATCATCNCGGNGCGGATGCTCATNCGGCGCATTTGCTCNAAT  
CGTTCCCGTATGCCACCTTGACGATGTCCTTCATATGGACCACGCCGATGGCCCNCGCGCTNCTG  
(SEQ ID NO. 538)

Clone Rv38

.....Rv38SP6.seq:.....  
CCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAG  
CTATTTAGGTGACACTATAGAATACTCAAGCTTCCACATCGGTATGCCAAAGCATTGCGCCGCTATCGATTTCCGCGCT  
GGCATCGCCAAGGTGGACTTCTTGCTCAGCGACGAGATCCCGTGGTCCGATCCGCGGCTGCGGCGGGCTGCGACCCCTG  
CATCTCGGCGGCACCCGTGACCAGATGGCGCGCGCCGAGGCGAGCGTCGCGGCGGGACGCCACGCCGACTGGCCGATG  
GTGCTGGCCGCGTGTCCGCACGTGCGCGACCCCGCGCGCATCGACGAAACCGGCGCGCGTCCGTTCTGGACCTATGCC  
CACGTGCCGTCGGGGTCCACGCTCGACGCGACCGAGACCGT (SEQ ID NO. 539)

.....Rv38T7.seq:.....  
CGCGTCCACCGCAGCGTGAGATTGGTGGCGCCATTTCGTCGTGGTGTAGCTGCTGTTGGCGGCGTCGCCGTATTGTGCG  
GGCCAGCCTTGTGCGGGGCGCCTTCTACCCACGAGTCGGCACTTCCGCAACCGCCAGCTCGACCGCGATTACGGCG  
GCCGCAACGGCCGCGGAAGGCGTCTCGCAAGCGCCTTATCCTTTTCGAGGTTCCAGATCCTTCCGCTACGTGGGTC  
GCTCATCGGCGGGCCCGCCGAATGAGTACAGGTGAGGGTAACCGCTACAAATGAAGTTGGTCAGTGCTGGCCAACTG  
TGTAATGGTTGCCCGGCTCGGGTCACCACGTACATTCTGGCAAGGCGGGCGAGATTGCGTTCCTCGCGTCTTGGCCG  
GTGGCGGTTCCCGGTTGTCCGTGGCGGTGTCGTGTACGTGGTGAAGTGTGCTGAACCTCCTCAGTTTGGGCT  
(SEQ ID NO. 540)

Clone Rv390

.....Rv390SP6.seq:.....  
CTCAAGCTTGCGTGGATCTGGCGGCTGAGCCTGTTCTTGGGCAACATGCCGAGGGATCGCCTTTTCCACCACGCGGT  
CGGGGTGGCGTTGCATTAGCTCACCGATGGTGCGCTTGTGCAGGCCGCCGGGATACCCCGAGTGCCGGTAACCATCT  
TGTGCTGCAGTTTGTGCGCGCTGATGGCGACCTTGTGCGCGTTGATCACNATGACNAAGTACCGCCATCGACATTGG  
GGCGAACGTGCGCTTGTGCTTGCCGCGCAGAGGTTGGCCGCCGCGACGGCAAGGCGGCCAANCACCACGT  
(SEQ ID NO. 541)

.....Rv390T7.seq:.....  
TTTGGGATGGGCAAAAAGGCGAAGCNC CGCTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGGCTAGGGCTTCTC  
GCGGGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGCTGCCCTCCGACCGGAACATTCGGGGATGGCAGCAACC  
TGGTAGCACCTGGCCGGGCGATGATCTGCAGCGTCGCCGCGGGTAGTCGCCGCCCGGGCGGCTACAGTCTGAAACGC  
GATGACCATCGATGTGTGGATGCAGCATCCGACGCAACGGTTCCTACACGGCGATATGTTGCGCTCGCTGCCCGGTG  
GACCGGTGGGTCTATCCCGA (SEQ ID NO. 542)

## Clone Rv391

.....Rv391SP6.seq:.....  
CTCAAGCTTCGTCATAAGACCATGGTGGCTTTCTTTACCCGTCANAGTCGGGGGCATCCGCACCGGCTCGCATCG  
CATCATCTCCACGACGGGCGCTCATCAGCTTGGGCCATTTCAATGTACTTGATACCCCGCGTGGGGTAGGCCA  
CTGCNACAATTCAAACACGGGTGTACACGGTGAATANTGTGNANATGGGCTCTGATCAACCGTCNAAACCCGGTTTC  
(SEQ ID NO. 543)

.....Rv391T7.seq:.....  
GAATTCTGCGTGACCGCTATGGGTTGCAGCAGCGGCTGGCGCCGCACACCCACTGGCCCGGGTGTTCGCCCCGA  
ACCCGGATCATGGTGAGCGAAAAGGAGATTGCGCTGTTCCGATGCTGGGATTGCGCCACCGCGAGGCCATCGACCGATTA  
CTCGCCACCGGGGTGCGAGAGGTGCCGAGTCCCGCTCCGTCGACGTCTCCGACGATCCATCCGGCTTCGCGCGTCGG  
GTGGCGGTAGCCGTCGATGAAATCGCTGCCGGCCGCTACCACAAGGTGATTCTGTCCCGTTGTGTGAAAGTGCCTTTC  
GCGATCGACTTTCGTTGACCTACCGGCTGGGGCGTCTGCACAACACCCCGGTGAGGTGCTTTTGTGCAAGTTGGG  
GGAATCCGTGCTCTGGGTTACAGCCCCGAACCTCGTCNCGCGGTGCGCGC (SEQ ID NO. 544)

## Clone Rv392

.....Rv392SP6.seq:.....  
GCAGTTGGGAATCGCTCTGCAGCAAACCANTATTCTGCGCGACGTTGAGAGGACTNNTTGAATGGACGGATCTACCT  
GCCGCGGACGAGCTGGACCGATTAGGCGTACNCTCCGCTGGACGACTCCGGGGCACTCGATGACCCCGACGGACG  
GCTCGCGGCACTGCTGCGGTTTANTGCCNACCGCGCCGANACTGGTATTGCTGGGACTGCGGCTGATTCCACACCT  
CGACCGCCGACGCGTGCCTGCTGTGCGGCCATGTCTGGCATCTACCGCCGTCNGCTCGCCTTGATCAGACCATCGCC  
GGCGGTGCTCTACCATCGGCGAATCTCTCTGTTGCGGACTGAANAANGCCCAAGTGGCGGCGGACGACTGGNCTCTT  
CGGTAACCTGCNGACCGCCATTGGACCGCTACCG (SEQ ID NO. 545)

.....Rv392T7.seq:.....  
TTGATCTGGACGCTGAGACGGTGATCGGNCCGAACCTGAATTGTCCGGTAATGCCAGCGCAGAAAGCANGGTGGTG  
GCCGGGGCGGTGAANCCGGCGTCGGCGGCACCGTCGAAGTCGATGTGGATTGCCGGAATGGGGATGTCCGGCACGGCG  
AAGCCGTAGTTGCTTGTCCCGTGAGGCCANGTGGATGGGGGAAGGATCGTGGTGTCCGGGATGATAATGGGGCCG  
ATGCCGCGGTTGAAGTCCAGTGGATCGGGAATTCGGGAATCGTGATGCCGACGTTAGGGCCGAACAGGCCCTCCAAG  
TTGCCTCGCCACNAGATGCCGTTGCTGAAGTTGCCGACATGAGGGCGCCGGTGTCCACATTGCCCGAATTGGCGACG  
CCGGTGTGGC (SEQ ID NO. 546)

## Clone Rv393

.....Rv393SP6.seq:.....  
CACGTAGGCGCGCTCCATAAATNACTCCGCCGCGCTTCGCACATCCTCGTANCGATCCTTGGCGAGCAGGTCAACCGG  
GCGCTGCCCCGTCNAGGAGCCGGTTTTTGGCGTGCAGCCACTGGCCGACACCTCGGGGGTAAGCGAATCCGAGAGCAG  
GAGGACNAGTCAAGAACTGCGCCAGCCGGTCTGACCGCTCAGGGCGGATGTGCGCGGTCCGCCACCCGCGTACCGC  
CCGATCGGACACCTGTATGACCGCGGCGACNTCGACCTGGGTGACGCCGAAGGGTTTCAGGGCATCNACNATCTCGCT  
GGCCTCGACCGCCCGGTCCAGGGTGACCGCCATCGTGGTTCCTCCGCAACTTCGGTTCTACTACCGTAAACGCTACC  
G (SEQ ID NO. 547)

.....Rv393T7.seq:.....  
CGGGGAACGGTCTCGCACACCTGGTTGCTGTTGCGGGAATTACTCGGACANCAAAACGTCAAGAACTACGACGGCAG  
TNGGACAGAAACGGTCCCTGGTGGGCGCCCCGATCGAGTTGGGAAGCTGATATGTGCTCTGGACCCAAGCAAGGAC  
TGACATTGCCGGCCAGCGTCGACCTGGAAAAAGAAACGGTGATCACCGGCCGCTAGTGGACGGTGACGGCCAGGCCG  
TGGGCGGCGGTTTCGTGCGGCTGCTGGGACNCTCCGACGAGTTACCGCCGGGAGGTGCTGGCGTGGCCACCGGG  
CGAATTTCCGGTCTTCGCCGCGCCCCGGGATCCTGGGACCGCNGGCGCGCTGTT (SEQ ID NO. 548)

## Clone Rv396

.....Rv396SP6.seq:.....  
CTCAAGCTTTGTCCGACAAGCGTTCCCGGGCGGTGACGAAGCGAACGTGCGTTGGCCCACTGCGGGTCGATATTGCCG  
CCAGGA (SEQ ID NO. 549)  
.....Rv396T7.seq:.....

CGTCAGCACGGCGACGTCGCGNTACGCCGAGCAGTTACACAATCGCTCTGCAGCAAACCAATATTCTGCGCGACGTTG  
GAGAGGACTTCTTGATTGGACTG (SEQ ID NO. 550)

Clone Rv39

.....Rv39SP6.seq.....  
CTGCATCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTAC  
GCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCGCGCAGCGCGGGTTGACCCGGTTACGCCGTCATAGC  
TGGCCAATCTGGCATCGTCGATCANCATGTGGTGGGGGGTGACCTCGGCGGTGATCGAAATACCCTGGTCCTTATCCC  
ATTTTCAGGATTCGACGGTGCCCGCGGGCCGACGCGTGACAGATGTGACCCGGGCGCGGGCGTCACGGGGCCAGCAAGG  
CGTCGCGGGGCGACGATCGATTCTCGGCGGGCCGCGGCCATCCCGCCAGGCCAGCCGCGCCGCCATGGGTCCCTCGT  
GCGCGACGGGCGCCGACCGTCAGCCGGGGCTCTCGGCGTGCTGGGCGATCAGCACGCCCAAACCGGTG

(SEQ ID NO. 551)

.....Rv39T7.seq.....  
CCGACGCGCACTACGTGCTGGTGCCACCCGCGACCCGACCGGCACGAGCTACGCAGCTACCGCATCGTCGATGGCG  
CTGTACCCGAGGAACCTGTCAATGTCTGTCGAGCAGTACTGAACCGTTCGAGAAAGGCCAGCATGAACGTACCGTAT  
CCATTCCGACCATCCTGCGGCCCCACACCGGCGGCCAGAGAGTGTCTCGGCCAGCGGCGATACCTTGGGTGCCGTCA  
TCAGCGACCTGGAGGCCAGCTATTGGGCAATTCGAGCGCCTGATGGACCCGTCTCCCGAGGTAAGTTGCACCGCT  
TCGTGAACATCTACGTCACGACGAAGACGTGCGGTTCTCCGGCGGCTTGGCCACCGCGATCGCTGACGGTGACTCGG  
TCACCATCCTCCCGCGCGTGGCCGGTGGGTGAGCGGACACATGACACGATACGACTCACTGTTGCATGCCTTG

(SEQ ID NO. 552)

Clone Rv3

.....Rv3SP6.seq.....  
TGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG  
CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGCCGGGAGGGTGCAATGGCCGACTCGGATTTACCCACCAAG  
GGGCGCCAACGCGGTGTCCGCGCCGTGAGCTGAACGTTGCTGCCCGCCTGGAGAACCTGGCGCTGCTGCGCACCCCTG  
GTCGGCGCCATCGGCACCTTCGAGGACCTGGATTTCGACGCGCGTGGCCGACCTGAGGTTGGCGGTGGACGANGTGTGC  
ACCCGGTTGATTTCGCTCGGCCTTGCCGGATGCCACCCTGCGCCTGGTGGTTCGATCCGCGAAAAGACGAAGTTGTGGTG  
GAGGCTTCTGCTGCCTGCGACACCCACGACGTGGTGGCACGGGACGCTTAGCTGGCATTCCT (SEQ ID NO. 553)

.....Rv3T7.seq.....  
GGAAACACCGNCGCCGTCGTGGCCACCAACACCGCGACCGAGCACCGTGACCCGGACCGGGGTGCCGCGGAACCGGTC  
TTGGCCAATTGCCGCGGCACCAAGCCGTGCGCGCCATGGCGAACAGCACGCGGCATTGCCCGAGCATCAACACCATC  
ACCACCGTGGTAAGCCCGGCCAGCGCGCCGACGGAGATGCGCGCTGGCCAGTACACCCCGTTGGCCTGGAACGCG  
GTGGCCAGATTTGCCGCCCCGCGGCCCGGTACGGTCCGAGATTGGGTGTATGGAACCATGCCCCGACAGCACCCCGAT  
ACCGCGACGTAGAGAAGGGTCACGACCCCCAGCGACGCGAGAATCCCTCGAGGGACGTCTCGTTGAGGACGCTTGGTC  
TCCTCGGCCATGGTGGCCACGATGTCAAACCCGATAAACCGGAAGAACACGATCGATGCCCGGCCAGCACGCCGTA

(SEQ ID NO. 554)

Clone Rv40

.....Rv40SP6.seq.....  
CCTGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTA  
CGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGTCTCGGGCGTGGCCTCGGCCAAGAAATCGTCGACGC  
CGGCCTCCTGTGCAATCGCCTTGGCGGTGCGCGGGTGTGTCACCGGTGATCATACGGTGCAGATGCTCATTCGGCGCA  
TTTCGTGCAAGCGTTCCCGTATGCCACCTTGACGATGTCTTCAGATGGACGACGCCGATGGCCCGCGCGCTGCTGT  
TATCGGTCCATTCGCAACGACTAGGGGTGTCCCCCGCGGAGCTGATGCCGTGACAAATGGCACCCACCTCCTCAG  
TGGGGTGGCCACCGTATCGCAAAACCACTTCATACCCGACCGCGGCACCTTGCGGATCCGAACGGATGCGCTC

(SEQ ID NO. 555)

.....Rv40T7.seq.....  
TTCGTTTCGATGGCGCCGCCCGGCTACGGTTTGACCTGTGGGTGTGCAATTGGGGTCAAATTCGAGGTGCGCGCGCT  
AAGAGTGGTCATCCTGCACCGCCCGGGGGCCGAACCTGCGCGGCTCACACCGCGCAACACCGACCGAGCTGCTGTTGCA  
CGGCCTGCCCTGGGTATCCCGCGCGCATGACGAGCACGACGAATTCGCCGAGCTGCTGGCTTCCCGCGGTGCGGAAGT  
GCTGTTGCTGTGCGACCTGTTGACTGAGGCACTACATCACAGCGGGGCGCCCGCATGCAGGGGATCGCCGCTGCCGT  
CGACGCACCGCGGCTGGGACTGCGCTGGCGCAAGAACTTTCGGCCTACCTGCGTATCTCGACCAAGCANGTTGGCG  
CATGTGCTGACGCCGGCATGACTTCAACGAACCTCCNTCCGACACGCGCAACGAAGTGTGCTTGGTGTGCGTATGC

(SEQ ID NO. 556)

Clone Rv412

.....Rv412SP6.seq.....  
GCGGCGAGTGTGGTGGGTGCCGAACACGAATCCAACGACGCACTGGCGGAGAGATACCACTTGCTGTACTGGAAGCAC  
GTGCTGATGATCTCCCGTGAATGTGCTCGCCGCCGTCTATCGAAAACAGTGAGCATGCTGCG (SEQ ID NO. 557)

.....Rv412T7.seq:.....  
CAACCGCGCTCGGCGCGCTCTGGGCCTTCCGCCGGCTCCGCCGACAATTCTATCTCTGGATCAGCGGGGCTCTCCGGGC  
CGGCCTCCGCGAACTCAACAGGCCGCGCCTTCCGGCCGAAACATTCCCTAGCCATATATGATCGCACCTCGATACAG  
ATCTGGCGGCAACACCGCAAAGCGTCCGACGGGCCAACCTCCGCAATTAGGTATCCGGG (SEQ ID NO. 558)

## Clone Rv413

.....Rv413SP6.seq:.....  
GAAGGTCTGGCGAAGGTGTGGCTGGNTGCCGATCACGAATCCAATGATGCAGTGGTCCGGAAGATATTAGCCACTTGCTG  
TTCTGGAGACAGGTGCTGATGATCTCCCGTGGAAATGTCCCTCGACTCCGTCTATCGAAATCTGTGAACA  
(SEQ ID NO. 559)

.....Rv413T7.seq:.....  
TCCTGCGCTCTGGGCCATTCTCGGGTCTGCCGACAATTCTATCTCTGGATCTGTGGGGCTCTCTTGGCCGGCCTCNGC  
GATCTCTTCANGGCGCGCCTTCCGGCCGAAACATTCCCTATCCATATATGATCGCACCTCTATACACCGTTTGGCGGC  
AACACCGCAAAGTGTCTGTCTG (SEQ ID NO. 560)

## Clone Rv414

.....Rv414SP6.seq:.....  
AGCTTTACGCTGGCGTATCAGCGTTGGGGCCGCTGCCATTTCGGTCCGCCAACGCGTTGCCAGCTCCCTGCGCTGTCA  
GGGCTTGCGGCCAACTGGCCACCGCAACAACTTGGCTGAGCTTGATC (SEQ ID NO. 561)

.....Rv414T7.seq:.....  
CTCTATCTGGCGTCACATTTCGCAATCTTTAGATTGCAGATATCGATAAAATCACCCGCGCGACAAGACCGCCATGTCA  
TCCTTTTCGATGTTATTTTCGCCGGCCTGGGGAAGCGCAACGACGTTGCCTACACGTTCCGCCGT (SEQ ID NO. 562)

## Clone Rv415

.....Rv415SP6.seq:.....  
AGCTTTNCCTTGCATCTGCACCCCGATCCAGTCAGCCAGTCGGCGTTCTCCACCAAGAAGTTGCGGGCATTTCTCCT  
TGCCCTGGCCGAGCTGCTCGCCCTCGTAGGTGAACAGGCCACCCGACTTGCGGATGAGGCCCTGATCCACACCCATGT  
CGATCAGCGAGCCCTCCCTGCTGATTCCCTTGCCGTAGAGGATGTGCAACTCGGCCTGCTTGAAGGGGGCGAACAGT  
TGTGCACGACAACCCCTTCGGCGACGAGGGTGTGCAATTCTTCGACCTCGAGGTCGAACGTTTCGTGCCCGCCGCGTTG  
GCAGCACTTCTCGGATCACGGAATAGCGGANTTCTTCGCCCAGCATGTGCTGCAGGAATTTGTCTACAGGGCATCCG  
CGAGCGCCTGCACGCG (SEQ ID NO. 563)

.....Rv415T7.seq:.....  
ACTGTCNAGGGAATGCTTCGCAGCATCTACCTGCAGTCGCTTGTGCATAAGCGGACGGCCCNACCTGTTCTGTTCCG  
GGACACCAGACGCGGGAGCACCGGCAGTACGGCGAAAGGTTTGAAGCGGAAGGAGTTGCGCAAATCGGGGCGCCCAAC  
ACCCGTCCGCAAGACGCGGTCAACGACCTGTTTCAGGCGATCAGGGTCACCGACTCACCTGCACTGAGAACAAGCGAT  
CTGCTGATCTGCCAGAAGATGGACATGAATGTCCACGGCAAGCCTGATGGCCTGCCGCTCTTCCGGGAATGTTTGGC  
(SEQ ID NO. 564)

## Clone Rv416

.....Rv416SP6.seq:.....  
TGAATTATGATCCCGACACAACCTGCATCANTTTAGCCGCGTCGNGATGCTATCCGCCGACGGTTTGGANCNGGTCCGT  
GTCGTTTCGTGTTGATCTACCCGAAGTTGTGTCCGCCGCCGCCGGGATCTAGCGAACGTGGGATCGACAATCAGCGC  
CGCCAACAAGGCGGCAGCGGCTGCGACCACGCAGGTGCTGGCCGCGGGCGCCGATNAGGTGTCAGCGGCATCGCGGC  
GCTGTTTGGTATGTACGGCTGNAATATCCGGCGATCAGTGCAGCAAGTTGCCGCGTATCACCANCAGTCCGTGCAG  
(SEQ ID NO. 565)

.....Rv416T7.seq:.....  
AACGGGGACCNCAAGAAACCATTCANAACGAGGGGTCTGCACCAACGTGAAACCGACGGTTGCCAGCCGGCCACG  
ATATTGCGTGCTCGAGGGTCCGCTGTACCCTCACCAGACGTGAGTCCACACCGCGGAGGGCGGCGACTCTGGCGTCTG  
TTAGCAGCCGAGCTCAAGGTGTCCCGCACTGTCTCGAATGCTTTAACCAGCCGGATCAGCTCTCCGCCGATCTA  
CGTGAACGAGTGCTTGGCACGGCCAAGCGACTGGGCTATGCCGGACCGGATCCGGTGGCGCGATCGTTGCGGACCCG  
AAAGCCGGTGCGGT (SEQ ID NO. 566)

## Clone Rv417

.....Rv417SP6.seq.....  
AGCTTTGGAGCCNCNCCGANCCNCCGGTACGCCCCGCCACCGCCGTACCCGGCACCAGCCCTTTGAGCCGTTGCGC  
GTGGCCGCGGTGGANCTGGCCGACGAGGGACTGATCGTGCTGGGCAAAGTGGTTCGATGGCAGCTGGCCGCGGATCTG  
AAGGTCGGCATGGAGATGGAGCTGACGACCATGCCGCTGTTCCGCCACNACGACGGTGTGCAGCGCATCGTCTACCG  
TGGCGGATCCCATCGCGCGCCGGCGACNATGCANAGCGCANCATGCTGAGGAGCGCGCCGATGAGGATGAGCGCGC  
CGGAACCCGTTTACNTCCTGGGTGCCGGTATGCACCCGTGGGGGAAATGGGGTAATGACTTC (SEQ ID NO. 567)

.....Rv417T7.seq.....  
TTCTCNCATCGTTCTGACTNNGATGGGACGCTGCTGCCGAGGCGATCCTGGCCAACCGGCTCTCGCCGGCGCTGACC  
TTCGGCGGGGCGAACCTGAACTTCTTTCCGATGGGCGCTTGGGCCAAACGTACCGGGGCTATCTTCATTGGCGCTCAG  
ACGAAAGATATTCCCGTCTACCGCTTCGTATTACGTGCTTACGCCGCGCAGCTGGTGAAAACCATGTCAACCTCACC  
TGGTCGATCGAAGGGGGTTCGACCAAGACGGGCAAGCTACGGCCACCGGTGTTCCGGATCCTGCGTTACATCACCGAT  
GCGGTCGACGAAATCGACGGTCCCGAAGTGATTTGGTGCCGACCTCGATCGTGTACGAACAGCTGCACGAAGTGGAA  
GCCATGACCACCGAAGCCTATGGCGCGGTGAA (SEQ ID NO. 568)

## Clone Rv418

.....Rv418SP6.seq.....  
TTCTTCCGGGTACCGCTGATCGGCGGCACCATCACGCACCCGGTGCAAGGCGAGGCGGCCGCGGTGTGGTGTGCTA  
CGGCCGCGCCAGCCCGGTACCGGTGTGATCGCCGGTGGTGCGGCCCGCGCGGTGCTGGAATGTGCGGGGGTGCACGAC  
ATCTTGGCCAAGTCGCTGGGCAGTGACAACCGCATCAATGTGGTGACGCCACCGTGGCCGCGCTCAAGCTGCTGCAC  
CGTCCGAGGAGGTGGCGGCGCGCCGCGTTTGCCAATAGAAGACGTCCCCCGCGCCGGGATGCTG (SEQ ID NO. 569)

.....Rv418T7.seq.....  
GTCGAAAGTGACCATCTCTACCTTGAGTGCCATACCGCCCCACCCTATGCCTCGGATAGCTCGGCGGAAAGAAACGCT  
TGCACTGCCCGCAATAGGCGGCTACGTCGTGAGCGCCCATCACTCTCGCGCGGAGTGCATCGCCAGCTGGGCGGCG  
CCGACGTCGACCGTGGGGATTCCGGTGCGCGCGCGCGGCCAACGGCCCGATCGTCGACCCGCACGGCAGATCGGCGCGA  
TGTTTCGTAACGCTGCATAGGCACTCCCGCGCGCTGGCAGGCCAGTTGCGAAACGCCCCGCGGGTGCTTCCGTCGG  
TTGGCTTTACCGCAAATTTGGGGTTGCCCT (SEQ ID NO. 570)

## Clone Rv419

.....Rv419SP6.seq.....  
AAAGCCACGGAAACGATTGCCTACTGCCGAATCGGGGAACGGTCTCGCACACCTGGTTCTGTTGCGGGAATTACTC  
GGACACCAAACGTCAGAAGTACGACGGCAGTTGGACAGAATACGGCTCCCTGGTGGGCGCCCCGATCGAGTTGGGA  
AACTGATATGTGCTCTGGACCCAAGCAAGGACTGACATTGCCGCCACGCTCTACCTGGAAAAA (SEQ ID NO. 571)

.....Rv419T7.seq.....  
TTTCGCCACCGCNAGGTCTGCGCTTCCAGAAAAGCGTGGTTTCGCCGGGCGCGAGGATTCGACGGTCCAACTGACC  
AGCCGGTCCCGCCACCGTTAGGCAAGATCGCGGTGTCTATATGTTCCGCCCTCGGCATAAACGCCATTGCTGCGGTGA  
AAATCGGACATCTCGCCGATTGCCACGTCTACATGATCCGCTTTGTCGCCGCGCGGGTCTTGACAAACGCGATGTCN  
GCCTCCTGGGAAGCGGTGGC (SEQ ID NO. 572)

## Clone Rv41

.....Rv41SP6.seq.....  
TCGCCAAGTGGATTCTGCTCACCNACGAGATCCGTGGTCCGATCCGCGNGCTGCGGCGGGCTGCGACCCTGCATCTCG  
GCGGCACCCGTGACCAAATGGCGCGCGCCGAAGCAGACGTCTCGCGGGGACGCCACGCCGACTGGCCGATGGTGTGG  
CCGCGTGTCCGNCGTNCCGACCCCGCGCATCNACCAAACCGGCCGCGCTCCGTTCTGGACCTATCCCACGTGCC  
NTCGGGGTCCACGCTCGACGCGACCGANAACGTAACCAGCGTCTCGANCGGTTGCCCCCGGCTTCCGTGACATCGT  
GGTGGCGGCCGCGCCGT (SEQ ID NO. 573)

.....Rv41T7.seq.....  
GTACCGTCAACATGATCGCCCCATCGGCATCGGTGAGCTGATAGATCCAGCCGGTTTCGCCAACCCCGGAGCGATC  
TTGGCGCGCTGCTNGTNGTCNCTGANACNTAGCCACCAACAGAGCCCGGTGTGCGACAAGANGACTGATCGGATCTCT  
CCGGACACNTCGAGGGGGTCTCAGGAGNCCGGGCGCCACCCGAGGTAAGCCTCCGCCAGCCTCACACCGCGACCG  
GGTATCNCAAGTCGCGCAATAANCCACCACTCCTCGGACCCACGTTGTATGCGGCTGGT (SEQ ID NO. 574)

## Clone Rv42

.....Rv42SP6.seq.....  
ATACTCAAGCTTAGACCTCACTGATGTGGCGGGACGCGGGAGATAACCGCGGTTTCGAGCCGTTCAACAGTGGTGGTTC  
CCACACCAAGTTGTTTGCCTTTGCGAAGTAAAGCGATTTCGATTTGCTCGAAAAGAGGGGCTGGCTGCTCGTGAGGGACAT  
CCATGGCCGATACCTCAGCGATCTCAACGGTCAAGCGACTGCATGTTTGGCGCAAGGTATCGCTAAGCATAGGTTTCGT  
GACGGATTTGACAGCAAGAGCTTTCCAAAGATTGCTGTCCACATANTGATTTCGCATCTCTACACCTCTTCGCCGGTGC  
TGTC AAGAGCCATTTCGAATCAGTTATCTCGCTCGTGCTTGGAANAAATTTCCAGCCTGCGTTGGACAAACCGCGTC  
GCCAAAGCGGT (SEQ ID NO. 575)

.....Rv42T7.seq.....  
AGCTTCCCGAGAAACAGTGCATTCCCTAAGCAGCCCGTTGTACGCGCGATGAGTGAAGAGTGCACGCAATCGCCGGAA  
TCCGGCAAAGCCCTGCACAAGCGAAATCAACCCGGAGGCTGACAAGGCAACGTCGGTGATCCGTACCGCCTGGTTGGA  
CAAACGGCAGAAGGGCGGCTCGTCCGGTCCATCTACGCCGAGCACACTGGTGATAGCGCGCATCGGCATCGGTGCGGC  
CACGGTGAGACGACGTCCGCGGGCGTCTGGGTGAGTAACCCGCCGACCACTTCTCGGGCAAGCTGGTCGACCATCGG  
GCGCCACGTCTCAACGCGCCACGCGCCATACCTGGTGCCAGTTGCTTGCGCATCCGGGTGTGCGCGGCGGATCGGA  
CGTCGAGAAACGCGAGCCACCCGTGAGAAGTGACCCACGGCGCTGGACACGTGTCTGTTAC (SEQ ID NO. 576)

## Clone Rv43

.....Rv43SP6.seq.....  
CGGCCGGGATGTGCGCAATGGCAGGTTGTGCGCCGGCTTGATGTGCGCGTTAGCGCCGATTCCACCACATCCCCTTG  
CGAAAGTCCGTTGGGTGCAATGATGTANCGCTTCTCCCATCGAGATAGTGAGCAACGCAATCCGTGCGGTACGGTT  
CGGGTCTACTCGATGTGCGCGACCTTGGCGTTGACACCATCTTTGTATGGCGGGCGAAAGTCGATCATCCGGTAAGC  
GCGCTTATGACCGCCGCTTTGTGCCNGGTGGTAATCCGGCCATGCGCGTTGCGTCCACCGCGACCGTGCAGCGGGCG  
CACCAGCGACNTCTCCGGGGTTGACCGGGTGATCTCGGCGAAATCAGATACGCTGGCGCCGCGACGACGAGGCGTCT  
GGGCTTGACTTGCGAATTGCCATGGTCTAATCAGGTCTTTCTCTCACCTCTCGTCGCCGGGCTAGGGCGCATTCCT  
GCTCCT (SEQ ID NO. 577)

.....Rv43T7.seq.....  
TAGCGGTGTAACCAACTCCCGGGTCACCACCGCAAACCTCTTGCGGCAACAGCACCGTCGACGCGTCAACCGGGCTG  
CCCGGAATCCTGTGGATGGGCATCGAGTGCATGGTCACGACGTCCCCGACGCGGCGGGTGGCAACGACAAGTGCCCG  
GATGCACCACAAATGACGGCCGCACACCGGTGGGGACGGCCAGCACGAGAGCCGTGTGCGCGAAGTCGACGCTAATGC  
CGTAGGCATTGGCCGTCAACAGGGCGACGCCCCGCGTACCACCGAGTCCACGGNGGTTGGGCGGTCTCCTCGGCCAA  
CCAGGCGTGAACCCGGCGGATCCGAATGCAGCAAGACCCGTGGGC (SEQ ID NO. 578)

## Clone Rv44

.....Rv44-2ndSP6.seq.....  
CCATTGGTCCGTTGTGCGCATACCANTACNACGCGCGGGCACCTGACGCGGCGGCGCAACCATTCGGTGGCCATCGC  
CATCGTCTGCCACCCGGTCAACGGACGCACCTTCTCCTGGCCGACCTAGTGCGCCACCCGCGCGCTTGCCTCCCAT  
CGATCCGGTCAACATGAGCAGCGCCAACACCGAGCGGTACATGACATCTGCTGTGGAACCAAGTGACANATTCGCCCGC  
CCATGATGATCNTCGACCGTCTCCGATTCCGGT (SEQ ID NO. 579)

.....Rv44-2ndT7.seq.....  
GCCGGCCTGGTCAAAGGGGCGTCCGAAGGANCCGGGCTGGGTAACAAGTTCCTGGCTCATATCCGCGAATGCGACGCC  
ATTTGTGAGGTGGTGGGGTGTTCGTGACGACNACGTGACTCATGTACCGGACGGGTGATCCCCAGTCCGACATT  
GAGGTGCTGAGACCGAGCTGATCCTGGCAGATCTGCAAACCTGGAGCGGGCCACGGGCGGGCTGGAGAANGAAGCN  
CGCACCAACAAGGCGCGCAAGCCGGTCTACGACCCGGC (SEQ ID NO. 580)

## Clone Rv45

.....Rv45SP6.seq.....  
GATCCACTGACCACGATGACATATCGAAATGCTCGACGATTCCGATGGCGATCAAGGCCACGATGCCCTGGCGGTTGG  
GCGGTATCTGGTGGATGGTGACCGCGGTAGGTTCCCGTGATCGTGTGACCCAGTCCACGCGATGGGCGGCGAGGT  
CGTCGGCACGATCACCCGCGCTNTGCCGCCGAGTGCGCCTCGAGTTTGGCGGCCAGCTCTCCCGGTAGAACTCTC  
ACCGTTGGTGGCGCGATCTTCTTANCGTCGCCGCGTGGTCAGGAAAGGTAAACAGCTACCGGGTTTCGGCGCTCG  
TCCGCCGGGATGAACGCATCTGCGAATCCGGGCTGGGATGCGAACAACGGACCTGTGCCG (SEQ ID NO. 581)

.....Rv45T7.seq.....  
TCTACTGCCGAATCGGGGAACGGTCTCGCCACCNNGTTGCTGTTGCCGGAATTACTCAGGACACCGAAACGTGAG  
AACTACGAGCGGAGTTGGACANAATACCGCTCCNNGTGGGCGCCCCATCGANTTGGGAAGCNAAATGTGCTCTGG  
ACCCACCCAAGAATGACATTGCCGGCGCCCTCCAACCTGGAAATAGAAACNGTGATCACCCGCGCGGTTCTTGGAAG

GAATGGCATGCCCTGGGCCGGGCGTTCTTCCGCTGCCGGACTCCTCCCACCAATTACCGCCGAAGGCGTCCCGTCT  
GC (SEQ ID NO. 582)

## Clone Rv46

.....Rv46SP6.seq:.....  
ATACTCAAGCTTCTGTACCGAAATCCCGCATGGGATAACGGGTTTAGATTTCGACAACGGGACCGTGTTTCTCAACA  
AGCCGGTCATCAGCTGGGCCGGCGACAACGGTATCTACTTCACCCGCTTTCGCCCCGT (SEQ ID NO. 583)

.....Rv46T7.seq:.....  
CTGGCTCAAGCGCTCGGCGCGCAGGTGAACCTCGGACCGGCTCGACGTCGCCGAACGCGAGGCGGTGCTGGCCCCAGCC  
GACGCCGTCGTCGCACATATCGGCACCGTGCACAAGTCTACAACAACGCCGGCATCGCGTACAACGGCAACGTCGACA  
AGTCGGAGTTCAGGACATCGAGCGCATCATCGACGTCGACTTCTGGGGCGTCCTCCACGGGCC (SEQ ID NO. 584)

## Clone Rv47

.....Rv47SP6.seq:.....  
CCGCCCTCCGCATTATGGGTCAAGAACCATCGGGTCGGACTTCTGGGCTTCCAACGCTCGCGCCGTCCCN  
(SEQ ID NO. 585)  
.....Rv47T7.seq:.....  
CCGTGGCACTGTGACACATATGCGCCGCTCCTCTCATCGCTGCGCTCGGCATCGTCGCCGGCGGTCATGGCGTCACC  
CTACCCAAAGCCGAACGCGAAACGAGAACGTGTTCATTATTAGGGTGTGAGCACCATAACAGATTGCTCACCAGGAA  
CTCAGCAGCACCGGGACGGATGTGCGCCACCACGCCCATCTGGGGTGGTAGCGGGGAAATACCGCTAACGCGGCTCC  
GGTGCCG (SEQ ID NO. 586)

## Clone Rv48

.....Rv48SP6.seq:.....  
TACTCAAGCTTGTCCAAATATCGAAGCGTCGGGTCGCGAGGCTCGGTGCGCAGCTCCAGCAAAACCCGCTCCACCCCT  
AGATGCCGGTATCCCTCAAGGTCTTTATCCGCCGCTTACCCCACTGGCACACGGTCACCGGCAGTCGCCCCCGGCC  
ATGGCGCGCAACCGCTGAAGCGGACCCGACAGCCGCTGCGGTGATGGACTGATCGCGATCCACCCGGCATTGAGCCGG  
GCTATCCGCGGGAAGTTCGCGCGTCCCCCGCCACATACAGCGGAGGATAGGGCTTTGTACCGGCTTCGGCCAGCAG  
TAGATCGGATCGAAGTCCACATATGTCCCATGGAATTCGCGCTGCTCCTGCGTTCAGATCTCGATTATCGCGCGCAAC  
CGCTCATCGATCACAGTCCGCGCACCGCAGGGTCCACACCATGGTTGGCGACTTCTTCGCGCAACCAGCCACACCCA  
CGCCGAAACGAAACCGTCCCTGCG (SEQ ID NO. 587)

.....Rv48T7.seq:.....  
CAGGCATGCAAGCTTGGCCAACCTCTCATCGGACTTGAAGGTGCCGTCTCGTTGGCGGCCCTGCTCCACGGCACGTT  
GATGGCACCAGGAATGTGTCCGGGCCGCTGGCTTTGTTCTGCGGCAGGTGCGCGGGGGCCAGGATCTTGCCGGAGAA  
CTCGTGGGAGAGCGCACGTCGATGAGGTTCTTGACGTTGATGGCCGCCAGGACCTCGTCGCGGAATGCCCGAATCGT  
GTTATCCGGCGGGGANGCGGTGTAGGAAGTACCAGGCCGCTGACCGGGTCGCTGGACAGCGGGCGTCCGTCGAGCTC  
C (SEQ ID NO. 588)

## Clone Rv49

.....Rv49SP6.seq:.....  
ATACTCAAGCTTCAAAACAGGCCTGTTGTGGGCGCACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAAGTGCGGCC  
CGCACCGCCGGCATCTCCCGGTACGCGAGGGCCGCGGCCCGCGCCGAGCGACGGCGTGTTCGCGCAGTTTCGCCGTCA  
ATGATGCTGACCTGATCGGCCACCCGGGCGGTCTCGGCGTCGTCCCGTTCACTAATCGCGGTGCTCAGCAGCGTCTCG  
ACAGCCACCACCCGAGTGGAGACCAGATGCNCCACCACGACCGCAGCGATGCCAGTCACCTCACCCGTCC  
(SEQ ID NO. 589)

.....Rv49T7.seq:.....  
CAGGCATGCAAGCTTTGCAAGTTGCTGAGTAATGTGCGCCAACGTCACCACAATCGCGATGAATTCAATCATGCCGCCC  
AGGGCGGCCAACCCTAATGGTGGCCGCGAGCGGCAGCTCGATCGCAGCGCGGAGGTTGCCGGCCGCCAGTTGATTCAG  
AACAGGGTGAGGTCATAGGCGGGCAGGATAGTGACGAAGGCAAGACCTAGATCTGCCGTGCGGAAGAAGAACGAGTAT  
CCGGTCGACACAACGGAAGCGAAAGTGTCCGCGATGTTGATGAGCGTCGCCGTTGTGGCGGCGGTGGCGGCGGTAGC  
ACCGTCCGCACATACCGCGGGAACGCGGGCATCCGAATTTGGGCGAGGTTGTTCAAGGCGGTGGCAACTCACCATGA  
ATCT (SEQ ID NO. 590)



## Clone Rv4

.....Rv4SP6.seq:.....  
CCGGCTCGTATGTTGTGTGGAATTGTGACCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAG  
CTATTTAGGTGACACTATAGAATACTCAAGCTTGGCCGAGGGCCGAGTTCGATTGGTCGCGGTGCGCTCGACAGTTAG  
CTTATGCAATGCTAACTTCGGGGCAAAGTTAGGCGGATCGGCCGATGGCGGGCGTAGGTGAAGGAGACAGCGGAGGC  
GTGGAGCGTGATGACATTGGCATGGTGGCCGCTTCCCCCGTCGCGTCTCGGGTAAATGGCAAGGTAGACGCTGACGTC  
GTCGGTCGATTTGCCACCTGCTGCCGTGCCCTGGGCATCGCGTTTACCAGCGTAAACGTCCGCCGGACCTGGCTGCC  
GCCCGGTCTGGTTTCGCCGCGCTGACCCGCGTCGCCCATGACAGTGCGACCCTGNACCGGGCTGGCC

(SEQ ID NO. 591)

.....Rv4T7.seq:.....

GTGTGCTGTCAATTCAGAGCTGAGCCTGATGCACTCAACTTACTGAGCATGCTAACGCTGGTCGTGCGGGTCTTGTTTC  
CCGCGTGTGCGCAGGGCACACGCTCGGGGCGTAGCTGGGAGAGGCCCGGTCAAGCCCGGAGAGCAGTGCTCAGTCCG  
CCAGCTTGACCGACTTTCGATGAGAACGCGCTTCTCGCCGATTGAAGTGGCGTGCTGACGGTTCGTGAGCAGCGCTC  
GCCGAGTGCGGCGCTGATTCTTTTCATCGAGCCAGGAGCGCATTCGTGTTTCGGCCGCTGCGGGTTCGGCCCCATCGT  
CGACGCGATCCGTCACCCACTCCTCGATCAGGTCTGCCTCATCGAACGGGCCAACGGTGCTGTCGGAGTAAGTGTGCG  
TGGGCACGCGAGCCGGGTGCTGTGGTACCCACCGTTGCATGAACAA

(SEQ ID NO. 592)

## Clone Rv50

.....Rv50SP6.seq:.....

ATACTCAAGCTTCACCAGGCGCGGCGCGGCCGCAAGCCAGGCAGCCGCGCTCGGCGCGTGGGGCCTTCCGC  
CGGCTCGGCCGACAGTTTCGATCTCTGGATCGGCGGGGCTCTCCGGGCGGCCCTCGGCGACCTCAGCGGGCCGCGCCTT  
CCGGCCGAACCATTCCTAGCCATAGATAACCGCACCTCAATGCACGGTTTGGCGGCAACCCGG

(SEQ ID NO. 593)

.....Rv50T7.seq:.....

AGCTTCCGTACGACCCGCCCTCGCCGGTGCCGGCGCCATCGGTTCATCGGATCTCATGACGACGTACGTAAGCCCCG  
TAGCCGCGAGCGGGCGGGTCAACTGGCGAGGCGGCGGCGACGTGACTGAGCTGGCCGAGCTGGACCGGTTACCGCG  
GAACTACCGTTCTCGCTCGACGACTTTCAGCAGCGGGCTTGACGCGCGTGGAACGCGGCCACGGTGTTGCTGGTGTG  
CGCGCCGACCGGCGCTGGCAAGACGGTGGTCG

(SEQ ID NO. 594)

## Clone Rv51

.....Rv51SP6.seq:.....

ATACTCAAGCTTGCCGGGACCGCGGAACAGAACCGGCGGTTCTACCGCGGTGTGCGGCCGGCGCGATATCGGCCTCC  
CGACTAACCGAACCCGATGTGGGCTCC

(SEQ ID NO. 595)

.....Rv51T7.seq:.....

ACGTTGGCTCTGCCGGAACGTATTTCCAGCGGCACGCATTTCGGCGTGGGTGCCGGGCGCCGAGTTGCGTCGCTGGGAT  
CACGCAGCAGTCGCCGGCGGCTGCCGTGGGCTATGAATTGCACCGAGCCGGAATCCNCAC

(SEQ ID NO. 596)

## Clone Rv52

.....Rv52SP6.seq:.....

ATACTCAAGCTTGTTCGATTCCGTGGCACTGTACAGATATGCGCCGCTCCTCCTCATCGCTGCGCTCGGCATCGTCG  
CCGGCGGTTCATGGCGTCACCTACCCAAAGCCGAACGCGAAACGAGAACGTGTTCCATTATTAGGGTGTGAGCACCAAT  
ACCAGATTGCTCACCAGGAACCTACGCAGCACCGGGACGGATGTCAGCCACCACCCCATCTGGGGTGGTAGCGGGGA

(SEQ ID NO. 597)

.....Rv52T7.seq:.....

CGTTGGTAGCCCGATATGCATAGTGATCTTACTGAACATGATTTCCATTATGGAGCCCGGGGTGCCGGCAGCGCGAA  
CGGTGCGCCGTGACAGCGGGCGGCACTGACCAGGGTGTTCGGGGCAACATCGGCCCGGCTTCGGATTCCGGTCCGG  
GTACCGGGCGACCCACCGCTTCGAGGTA

(SEQ ID NO. 598)

## Clone Rv53

.....Rv53SP6.seq:.....

ATACTCAAGCTTGGCCAACTCCTCATCGGACTTGAAGGTGCCGTCTCGTTGGCGGCCCTGCTCCACGGCACGTTGAT  
GGCACCAGGAATGTGTCCGGGCGCTGGCTTTGTTCTGCGGCAGGTGCGCGGGGGCCATGATCTTGCCGGAAAACTC  
GTCGGGAGAGCGCACGTGATGAGGTTCTTGACGTTGATGGCCGCCAGGACCTCGTCGCGGAATGCCCGAATCGTGTT  
ATCCGGCGGGGAGGCGGTGATGAGGTACCGGCCGGCTGACCGGGTTCGTTGACAGCGGGCGTCCGTCCAGCTCCCA  
CTTCTTGCGGGCGCCGTCCAACNACTTGACTTCTCCTGG

(SEQ ID NO. 599)

.....Rv53T7.seq:.....

ATATCTTAAGCGTCGGGTCCCGAGGCTCGGTGGCAGCTCCAGCAAAACCCGCTCCACCCCTAGATGCCGGTATCCCT  
CAAGGTCTTTAGCCGCGCTTACCCCACTGGCACACGGTCACCGGCACGTGCCCCCGGCCATGGCGCGCAACCGCT  
GAAGCGGACCCGACAGCCGCTGCGGTGATGGACTGATCGCGATCCACCCGGCATTGAGCCGGGCTATCCGCGGGAAGT  
TCGCCGGTCCCCCGCCACATACAGCGGAGGATAGGGCTTTGTACCGGCTTCGGCCAGCAGTAGATCGGATCGAAGT  
CCACATATGTCCCATGGAATCCGCCTGCTCCTGCGTCCAGATCTCGATTATCGCGCGCAACCGCTCATCGATCACAC  
GTCCGCGCACCGCAGGGTCCACACCATGGTTGGCGACTTCTTCGCGCA (SEQ ID NO. 600)

## Clone Rv54

.....Rv54SP6.seq:.....  
ATACTCAAGCTTGTGCGGTAAACCCGACAGGGCGGTGGGTGCGGTGTCAAAAACAACCACACTTCTTTGCGGTTC  
GGTGATCTCGACACCGGCCGAGCCGACCACCATGCGCGCTAAATCGGCGATCAGCGCGTCGGCTATCGCCTGGGT  
GCCGCCACCGGAATCGGCCAGCCGACCGAATGGGCCAGCGTTGCCAGCATCAGTCCGGCGCCGGCCGACACCAGTGA  
CGGCAACGGTGAAATCGCGTGGCGGGCAACGCCGGTGAACAACGCGCGGGCATCCTCGCCCGCCAGCGACCGCCAGGC  
AGGGGTGCCCTGGGCCAGCATCCGCAGCCGAGACGCGAGGCCGAGCCAGTGCAGTAGGCAAAGACCGCTTGTGCGGA  
GACATGAACTCCACGACCGT (SEQ ID NO. 601)

.....Rv54T7.seq:.....  
AGCTTATTGAACCGCGGTGCGAGGCAAGTGGACCTCATAACGACTCGGGTCCAGCGACCGCGCAACACGAACGGC  
CGGACGACGTGGGCCAGGGTCGCGGCCTCCCCTACAAACAGGATCCGTTGCCTGCGAGCGACAGGCTCCGGTGC GGCG  
TTGGCGCCGCTGCTCGTCCAGCGTCCGGTCCCGGGTCCGCCGCGACGCTTGTTTCCTCCATACTCGCCCCCTAATCT  
CGAGGCAGCCCGTACCCGCGAGGCAACCTCCCAAAATGCAATCCCCCAAATGCAATGCGTCGAGCTATTTCTCACAC  
CGACCGCTAGTTGCGGATCAGAAATCCGTTGGGCGCGGAAGTCCAGCCGAATTTGTTCTCCCGCTCCGCATCATGCTT  
GTAATCGTTTGAAATTCATCTCATATGCCTCGATCGCTTCATAGGGTCCAGGCCAAACCGGGCA (SEQ ID NO. 602)

## Clone Rv55

.....Rv55SP6.seq:.....  
CTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCC  
AAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGCCACCTCGCGGTGTGTGGTGGAACCCATCTGAGCAGTGTG  
CCAAACCGGGGACAGACAGTCCCAATTGACGTGAGCCCGTCACTTGCTGGGTAAAGCGTCG (SEQ ID NO. 603)

.....Rv55T7.seq:.....  
TAGCGCCCCCTCCCGGGCGGAGCTCCACGGCGTGGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGC  
CCGGCTTGATGTCGGCGTTAGCGCCGGATTCCACCACATCCCCTTGCGAAAGTCCGTTGGGTGCAATGATGTAGCGCT  
TCTCCCCATCGAGATAGTGGAGCAACGCAATCCGTGCGGTACGGTTCCGGTCTGACTCGATGTGCGCGACCTTGGCGT  
TGACACCATCTTTGTCATTGCGGCGAAAGTCGATCATCCGGTAAGCGCGCTTATGACCGCCGCTTTGTGCCGGGTGG  
TAATCCGGCCATGCGCGTTGCGTCCACCGCGACCGTGCAGCGGGCGCACACGCGACTTCTCCGGGGTTGACCGGGTGA  
TCTCGGCGAAATCAGATACGCTGGCGCCGCGACGACCAAGCGTCGTGGGCTTGTTCTTGCGAATTGCATGTCTAATCA  
GGTCTTTCTC (SEQ ID NO. 604)

## Clone Rv56

.....Rv56SP6.seq:.....  
TGAAACTATATAATACTCAAGCTTGCCAAAGAAGACCTCGTCGACCAAGCAGGACGCGACCGTCGAGGTGGCGATCCG  
GCTTGGCGTCGACCCGCGTAAGGCAAACAGATGGTTGCGGGCACGGTCAACCTGCCACACGGCACTGGTAAGACTGC  
CCGCGTCGCGGTATTGCGGTTGGTGAAAAGGCCGATGCTGCCGTTGCCGCGGGGGCGGATGTTGTGCGGGAGTGACGA  
TCTGATCGAAAGGATTCAGGGCGGCTGGCTGGAATTCGATGCCGCGATCGCGACACCGGATCAGATGGCCAAAGTCGG  
TCGCATCGCTCGGGTGTGGGTCCGCGCGGCCTGATGCCCAACCCGAAAACCGGCACCGTCACCGCCGACGTCGCCAA  
GGCGCTCGCGGACATCAAGGGCGGCAAGATCAACTTCCGGTTGACAAGCAGGCCAACCTGCACTTCTC (SEQ ID NO. 605)

.....Rv56T7.seq:.....  
GCTGAGCTCCACGGCGTGGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTCGGC  
GTTAGCGCCGGATTCCACCACATCCCCTTGCGAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCCATCGAGATA  
GTGGAGCAACGCAATCCGTGCGGTACGGTTCCGGTCTGACTCGATGTGCGCGACCTTGGCGTTGACACCATCTTTGTC  
ATTGCGGCGAAAGTCGATCATCCGGTAAGCGCGCTTATGACCGCCGCTTTGTGCCGGGTGGTAATCCGGCCATGCGC  
GTTGCGTCCACCGCGACCGTGCAGCGGGCGCACACGCGACTTCTCCGGGGTTGACCGGGTGATCTCGGCGAAATCAGA  
TAGCTGGCGCCGCGACGACAGGCGTCGTGGGCTTGACTTGCGAATTGCCATGTCTAATCAGGTCTTTCTCT (SEQ ID NO. 606)

## Clone Rv57

.....Rv57SP6.seq:.....  
ATACTCAAGCTTGTGGTGACCTCGCCGGCGAACAGTTCTCGCACGATTTCCGGATTAGCGGGACTGGTCACCAAGTTG  
GGTATGCGGGGAAGGCGCTGACGTTCCGCCGCGATTAGCTGTTTATGACGCGGGCGGTGATGTCCTGATCACGGAAGTG  
GCTGTAATAGCCCAGGGTCGCCACGCTTCCATCCGGGCCCGACCCGGC (SEQ ID NO. 607)

.....Rv57T7.seq:.....  
GATGATCGCCGGTGCCACCCGATCCGTGCCTCGGTACGCGCAACGTGCTTTCCGGTCCGGCGACCAACCATGTCGCA  
CGCACCGACCAAGCCGAACCCGCCGGCCCGCACATGCCCGTTGATGGCGCCGACCAACCGGCAGCGGCGACTCGACGAT  
GGCGCGCAACAGCGCCGTCAATTCGCCGCGCCCGGCCACCGCCATCCGGTACGGATCACCACCACCTCCGCCGGCCTC  
GCTGAGGTCC (SEQ ID NO. 608)

## Clone Rv58

.....Rv58SP6.seq:.....  
ATACTCAAGCTTGCCGCAATCGAAACCAACCTGTTTGTGCCGCAAGAAATTACGCCGTGGCCCGGCGCCGATCAAGAA  
ACGCCCCGGCGCGCGGGCGGTGTGTCGTATGGCATGACGGGCACCAATGTGCACGCCATTGTCGAGCAGGCACCGGTG  
CCAGCCCCCGAATCCGTTGCACCAAGGCGACACCCGGCCACACCCGGTATCGACGGCGCGCTGCTGTTCCGCGCTGTG  
GCCAGCTCGCAGGACGCGCTGCGGCAACCGCCGCGCGGTGGCCGATTGGGTCT (SEQ ID NO. 609)

.....Rv58T7.seq:.....  
TTGGCGGGTTGGCCACANCCCGCGGTGACGGCGACGATGCTGGGCTGGTTGCGGCCCTGCGCCACCGCGGCTTG  
CATGCTGGTTGGCTGTCTTGGGACGATCCCGAAATAGTCCACGCGGATCTGGTGATTTTGGCGGCTACCCGCGATTAC  
CCCGCGCGGCTCGACGAGTTTGGCCTGGACTACCCGCGTGGCCAATCTGCTGAACCTCGCGGCCGGTGGTGGCCTGG  
AATGTCCANCGCGGTTACCTACGTGACCTTGATGGGATCCGGGGGNT (SEQ ID NO. 610)

## Clone Rv59

.....Rv59SP6.seq:.....  
NCGTGGACACCGGTGTGANCGCCACCAAGCCGATGTCTGCANGTCNATTCCGTCTCGGCAACATCTTGAATGCCGA  
GCAGCGCCTGGGCGTGATCGGCAACCGGGGATGACCGCTCGCCGATCCGCTCGACAATCCCGCGGGCACGTGACATGC  
CGGCGGACGGCTCGACGAGCTGGAACCTTACGCGACGACGATCCCGAATTGATCACCAGCAGGCTGCTACTCATGGACC  
CCTGCGCCTGAATCCCGTGATGGCCACGGTGTTGACTATTCTGTCGACAGTGCACCCGAGATAGTCTTACGGCTGCGT  
(SEQ ID NO. 611)

.....Rv59T7.seq:.....  
CATGTATTGCCGTGCTCACGGCGCCACGCTCGATGGTTTCTCGAAGTCTCCGGGCTGGTGACAGCTTCTCGTTGATC  
TCGTTTCGCCACGCCGTCTCTTCCCGCCGACGACCCGATCTCGATCTCCANAATGATCTTGGCGGGCCGCCCGCCTT  
GAGCAGCTCCTGGGCGATGGCCAGGTTCTCATCGATGGGCACTGCCGACCGTCCCACATGTGCGACGGAACAAAGATG  
TCACCTTGCTCACGCGTGCGCNAGATCNCANAAGGGCGGACATACTGTCTACTTGTCTTGGGCAAGTGGTCCGTGTC  
AGCCACGTCACGGGTACTTGGCGCGATAACGTGGTG (SEQ ID NO. 612)

## Clone Rv5

.....Rv5SP6.seq:.....  
GCCACCACGACCCGGCGTAACCTGCTCACGGAATGCGGCCAGGCCGCGGTAGCACGTGGTATCCGCCATAAAGG  
TGCACCTTAAGCACGGCGTCCCAATTCTCGAACGACATCTTGTGGAAGGTGCCGTGCGCGAAGATCCCGGCGTTGCTC  
ACCACACCGTGACGGCGCCGAATTCGTCAAGCGCGGTCTTGATGATGTTGCTGCGCCGTCTCGGTGGCGACGCTG  
TCCTTAGTTGGCGACCGCCCGCCCCCTTGTGCGGAATCTCGGCGACGACCTCATCGGCCATCGCCGAACGGCGCCC  
GTGCCCCGTGCGGGGCGCCACCGAGGTCGTTGACCAGTA (SEQ ID NO. 613)

.....Rv5T7.seq:.....  
CAGGCATGCAACCTTTGTCCACACGGCGTCTACTCCGTGCAAGGTCCGACCGCTTCCACGTCCCGCCGTGACGGTGCT  
CCATCTCCCTCAGCAACGCGTGAAGTGGTCCGATCCCGCGGCTTCAGG (SEQ ID NO. 614)

## Clone Rv60

.....Rv60SP6.seq:.....  
GTTGAGACGCAACCAGCGCACAAACGACGATTTGGCGTAGCGGCGGACGTCTGCTCGATTGATCACGTGCGGCTCGCA  
TCGAGCATGGCCCGCGACGCTACACGATCGCCGTGCTCGATGACACGACCGAGCCGTACGCCGGCCGTAAGCCGCGCC  
AGGATTGGCGGAAAAACGTCTACGTGGCGGGTGACTGGGTGTCGAATGATTCTGTTGGGTGCGTATGCGTCTGCAAT  
CGTCGACATAGATCCGTGCGCGCATCGCTCGACAACCTCCGGGTGAGTGGGAATACACTTGGCGATCACGCGACGTGCG

CGGATCGATGCCGACCGAAATACGACCACATGGCTCTTGTTGCNCAGTGTGGCGGCATCAAATACCCTCAGTGCCGT  
CCGAC (SEQ ID NO. 615)

.....Rv60T7.seq.....  
TTNCCGCCTTNACGCCTACTCCNAGACGATGCTCGACGCGTGTGAGCACACGGCGCTGCTGTAGACGGCACGGCGCAG  
CTGGATCGCGCTTGGTGCACCCAAGCCTCTACGCGCGTGCCTGCGTCATCGGGTACCGAACATATTCCGGTCTGT  
GCGCAGAGTGTGCATGTGCGGCTCTTGTGAACGAACATAGCAAAGCGTATATGTCTGTGGCGGCTCTGCAGATATCGC  
GATAATACGTATATACATAAGGTGGCGCGCATCTATCGGTATATCCGTTATGGCGGACGTGCGTGAGCGTGAGTCGC  
GGCGCATCGCGCACTTCGCGATCGCGTGACTGGTCTCGCGACTGCGCGCATGCGTAGC (SEQ ID NO. 616)

Clone Rv61

.....Rv61SP6.seq.....  
GGTGATGACGCACTTGCTTCGAATGAGTCATTGACTACTCCCCTGGTTGCTCTGCGATGGTGGAGTGCCGCGCAGCCT  
TGCCCGANGTCGCGATCGCGTGCAGGGCTTCGGGGAGCAGACTGACCTGCAGATGGAAGTCGTGCCACATGCCCGCGA  
ACGGCGAGCTCGATGCTTGTTCGAAGNGCGCANGCGGTTTCGATCTTGTCCGCGTCAACGCAGATCGGATCTCGCC  
GCGGTCTGCATGACGATGGCGCAGGCCCGCTCATGTCCCGTAGACGGGGAGATACGGGCAGCCGCGGATCGAGACCT  
ACGTAGCGCGGCGCCCATCGTGCCATCGACGAAGAATGACGGATCGCGCAGCGCCGTGCGTCTCGATGTACGC  
GAGATCGCCACGGCAGATCAGCGATGCGCGGGC (SEQ ID NO. 617)

.....Rv61T7.seq.....  
CGGTACGCGCGCAACAAACGCCTTGTGACGAGCGCGTCCGAGCGGTCTCGGCCCTCCACCGTCATGCACAGCTCCTTC  
TCCAGGTCTACGCCGACGTGCGGTCACATTGGTGAGCTTGGCGAATGCCCTCGGCAACCTCGTCGAAATGCGCCTCC  
GCGTCCGCATCGAAGGTGCGCATGTCAAAGATCAACTCGACGTAGTAGCTAGTTACCGCATCAGGTCACTGTTTGCTG  
GCCTCGGAGTCCGGCCGAACAATGGCCATTTCCCGCGACTCTAGAATCCAGTCATCGTCTCGGTGACGACGCCTTGCC  
GATCACATAGCTCGACCGGATCGGAGAGAATCTGTTCTCGT (SEQ ID NO. 618)

Clone Rv62

.....Rv62SP6.seq.....  
ATACTCAAGCTTAAGCGCAGCAGTACCGCGGTGCCTGGGCATCCCAGCAAACGGGGAGCTCAACGAACGATTCTTG  
AACGAAGGTCGTCCACCAACCTCCAAACCGAACGGTTGCCAGCCCCGGC (SEQ ID NO. 619)

.....Rv62T7.seq.....  
GCAAGTCCGCTCAATGTGGTTGTGATCACANGACTACGTGCGCTCAATCAGCTCAAACGTCAACCCGTGGCGTGCTGC  
GCAGCATGAAGGTGCGCGCCCGCACGATGTGGGCGAAGCAACAGGTAATAACTGGTCGGCATGGGTCAACCCCTCATTG  
GGCCGTTGCGGATCGGGTGACGCCCCGAGTGCCGGTCAACTCAACACCGCCTTACCAGATCTTTTCGTGAAAATG  
GCGGTGCTGCGGGTATACGTCCGCGATCCCACGAGGCGGAATCCGCTGAGCCGCACTGA (SEQ ID NO. 620)

Clone Rv63

.....Rv63SP6.seq.....  
ATACTCAAGCTTCGCGCCCTCAAGCGGCTGAAGGTGGTTCCGGCGTNCCAACNGTCGGGCAACTCGCCGATGGGCATG  
GTGCTCGACNCCGTCCCGGTGATCCCGCCGGAGCTGCGCCGATGGTGCAGCTCGACGGCGCCGGTTGCCNCGTCC  
GACTTGAACGACCTGTACCGCAGGGTGATCAACCGCNACNNCNGNTGAAAAGGCTGATCGATCTGGGTGCGCCGGAA  
ATCATCGTCAACAACNAGAACGGATGCTGCNNGAATCCGTGGACGCGCTGTTTCGACAATGGCCGCGCGCGGCCG  
GTCACCGGGCGGGCAACCGTCCGCTCAAGTCGCTTCCGATCTGCTCA (SEQ ID NO. 621)

.....Rv63T7.seq.....  
TGCGCATGGCAGTTGTTGCCGGCTTGAGTCGCGTTAGCGCGGATTCCACCACATCCCTTGCGAAGTCGTGGGTGCAAT  
GATGTAGCGCTTCTCCCATCGAGATAGTGGAGCAACGCAATCCGTGCGTACGTTGGGTGCTACTCGAGTGCGCANCTT  
GGCGTTGACACCATCTTTGTATTGCGGCGAAGTCGATCATCCGGTAAGCGCGCTTATCGACGCCGCTCTGTGCCGG  
GTGGTAATCCGGCCATGCGCTTGCCTCCACCGCGACGTGCAGCGGGCGCACACCGACTTCTCCGGGTGACGGGTGATC  
TCGGCGAATCAGAACCTGGCGCGCGACACAGCGTCGTGGCTGTACTTGC (SEQ ID NO. 622)

Clone Rv64

.....Rv64SP6.seq.....  
TGGGTGATCAGATACTGGCTAGTTGGTTCGGGTGGGGTGATCGAAGATCGCGGTGGCCGGCAGCGTTACTGCGGTGACG  
CTGTTAAGCGGTTACGTACTCCACGGCACTCAANGAATTANATCCGAATCGGCAAACCTGGCCAGCGTCGAGTCCG  
CAGCGCCGTGCGCGCCCCCACCCTGCGGCATGCTCACATAACACCTCGATCGCTGCGGGAGTTGCTCGTCCGCCGAC  
CGACCGGCCAGCCGGGCGGCAACCGGAGGACCAAGATTAGACACCACCATCGCTAGCCCGATCTGGCGCGCGGTGG  
(SEQ ID NO. 623)

.....Rv64T7.seq:.....  
TCGTAGCGGTTGCGACCANTCCGCGGACAGCTCCGCCACGCGACGGGTCGGGATCACCGCGGTCAAACCACCGAGCGG  
CGAGGATCTCTGGCCGTCGACGTGACCGCGCACGGCCGCGGTGATGGCCAGTCCCGACCGCCGTTCCACTTGGCGTAC  
GCGCTGGATGTGTGTGCCGCAACGGAATCCCACCTCAATTATGACCTCGTTGTGGGCGAGCGCGGTATCGTACGCCC  
GACCAGGAATCGTCGATGCTATCTCACGTACCGAAGGCCTCTCCAGCACACCGCATCCAGAACGTGCACACNGTCG  
ACATGTCTCGGCGGATCCGCCTGCAGAACGAACGCCANGTGCGCTGTGCGACACGGGTCGCGATCACCGCTCGCACGC  
GGAGATCGGCACACGCGCAGCGCATCGATCATAATCTCTCGATGCGGTCTCCACCACCGAACAG

(SEQ ID NO. 624)

## Clone Rv65

.....Rv65SP6.seq:.....  
ATACTCAAGCTTCGTTGAGGTGGTGGGGCAGATCACGTCACCGCACCGCTGTGCGGTGGCGCTGGATGCCGGCCGGAT  
CAACCACGCGTACCTGTTCTCTGGGCCGCGTGGCTGCGGAAAGACGTCGTCAGCGCGTATCCTGGCNCGGTTCGTTGAA  
CTGTGCGCAGGGCCCTACCGCCAACCCGTGCGGGGTCTGCGAATCCTGCGTTTCGTTGGCGCCCAACGCCCCGGCAG  
CATCGACGTGGTAGAGCTGGATGCCGCCAGCCACGGCGCGTGGACGACACCCGCGAGCTGCGGGACCGCGCGTTCTA  
TGCGCCGGTCCACTCACGGTACCGGGTATTTATCGTCGACGAGGCGCACATGGT

(SEQ ID NO. 625)

.....Rv65T7.seq:.....  
GCACTCACGCTGGTACAAGACCTTCACAAAATCTGAAATCCTGACCCGATACTTGAACCTGGTCTCGTTCGGCAATAA  
CTCGTTTCGGCGTGCGAGGACGCGCGCAAACGTAATTCGGCATCAACGCGTCCGACCTGAATTGGCAGCAAGCGGCGCT  
GCTGGCCGGCATGGTGCAATCGACCAGCACGCTCAACCCGTACACCAACCCGACGGCGCGCTGGCCCGGCGGAACGT  
GGTCTTCGACACCATGATCAGAACCTTCCCGGGGAGGCGGAGGCGTTGCGTGCCGCCAAGGCCGATCCGCTGGGGGT  
ACTGCCGAGCCCAATGAGTTGCCGCGCGGCTGCATCGCGGCCGCGACCG

(SEQ ID NO. 626)

## Clone Rv66

.....Rv66SP6.seq:.....  
ATACTCAAGCTTGTATAAAAAGATCGGTGAGCGCATCGATTGCTCCGCCGGGTTTGCCGCTGCGGCGGCGGAGCTGC  
CGTGACCGTCTATTTGGGTGATCAGATACTGGGCTAGTTGCGTCCGGGTGGGGTGATCGAAGATCGCGGTGGCCGGCA  
GCGTTACTGCGGTGACGGCTGTTAAGCGGTTACGTACCTCCACGGCACTCAAGGAATTAAATCCCGAATCGGCAAACG  
CCTGGCCAGCGTCAATCCGGCAGCGCCGTGCGGCCCCAGCACCGCTGCGGCATGCTCACATACCACCTCCATCGCTG  
CGGCGAATTGCTCGTCGGCCGACCGACCGGCCAGCCGGGCGGCAAACCCGGAAGA

(SEQ ID NO. 627)

.....Rv66T7.seq:.....  
CCTCATCATATGCCGATAGAGCTCTACATATTCAGGAGATCACCATGGCTCGTGCGGTTCGGGATCGACTCGGGACCAC  
CAACTCCGTCGTCCTCGGTTCTGGAANGTGGCGACCNCGTCGTCGTCGCAACTCCGGAGGGCTCCAGGACCACCGCTC  
AATTGTGCGGTCGCCCGCAACGGTGAGGTGCTGGTCNGCCAGCCCGCCAGAACAGGCAGTGACCAACGTCGATCGC  
ACCGTGCGCTCGGTCAAGCGACCATGGGCAGCGACTGGTCCATAGAGATTGACGCAAGAAATACACGCCCCGAGATCT  
CGCCGATTCTGATGAACGACGCGACCCGAGGCTACTCGGTGANGACATNACGACGCGTTATCACACCCCGCCTNC  
TTCAATGACCCACGTCNGGCACCAAGGACCCGGCAATCGCGGCTCACTTGNGCGATNGTCNACAACCAACGCGNCGC  
CTGGCTACGGGCTCAACAAGGCANAAGACACAATCCGCTCTCGATTGGTG

(SEQ ID NO. 628)

## Clone Rv67

.....Rv67SP6.seq:.....  
ATACTCAAGCTTATCGAGGCGCGCATACCGAAGCGTGGGAAATCCAGACCGAATACCGCGACGTGCTGGACACTTTG  
GCCGGCGAGCTGCTGGAAAAGGAGACCTGCACCGACCCGAGCTGGAAAGCATCTTCGCTGACGTGAAAAGCGGCCG  
CGGCTCACCATGTTTCGACAACTTCGGTGGCCGGATCCCGTCGGACAAACCGCCCATCAAGACACCCGGCGAGCTCGCG  
ATCGAACGCGGCGAACCTTGCCCCAGCCGGTCCCGAGCCGGCGTTCAAGGCGGCGATTGCGCATGCTACCCAAGCC  
GCTGAGGCGGCCGGTCCGACCCGGCCAAACCGGGCACGGCGCAACGGTTCGCCCGCCGGCACCAACCGGTCCGGTGA  
CCGAGTACGGTCCCCCAGCCTGACTACCGTGCCCCGGCGGGCT

(SEQ ID NO. 629)

.....Rv67T7.seq:.....  
TGGCCGGGCTGGTAGCCCGGTATGGCAAGGTTCCGCTCAATGTGGTTGTGATGCAGCAGGACTACGTTCCGCTCAAT  
CAGCTCAAACGTCACCCCGTGCGGTGCTGCGCAGCATGAAGGTTCGGCGCCCGCACGATGTGGGCGAAGGCAACAGGT  
AAGAACCTGGTCGGCATGGTTCGAGCCCTCATTGGGCGGTTGCGGATCGGGTTGCAGCGCGCCGGAGTGCCGGTCGAA  
CTCAACACCGCCTTCACCGATCTTTTCGTCGAAAATGGCGTCGTGTCCGGGGTATACGTCCGCGATTCCACAGAGGCG  
GAATCCGCTGAGCCGAGCTGATCCGGGCTCGCCGCGGCGTGATCCTGGCTGTGGTGGTTTCGAGCATAACGAGCAG  
ATGCGAAT

(SEQ ID NO. 630)

## Clone Rv68

.....Rv68SP6.seq:.....  
GTCCAGTCAAGCATCGGTCTCTCCGACTACGCCAAGANTGGCGACGTGTCAAGTGCANACAGCGGANATGGTGGCGCC  
TATGCGTCGACGCTCACAAACNGCGGTGANCGCGTTCTGGTCTGCACCATCGAGCCGTGCCAGCCCGCGCGTGGC  
GTCAGCCGCATCCACTGGATGCCTTCTCGGNGTTTCAATCANGTACANGCGACGTTCCGCCACCATCGTGCCGGGGCAC  
GGTTAGCGAGAAACCGCGACTTCACCGATTGCCTCGGTGATGCCGTGGAACAGATCGGGCCTATTGTGACAGCCAG  
TGTGATNCGTATTTGCCGCCGTGCTCCTCGTCGCAACGATGCGAACACAGATCCGTGGNGGACGATAGCGGCTGACAA  
NGTGGGGGCAACACAATCACATGCCACATTTCTTCATTTACGCCCCACAACCCAGACTTCGTCTCGATGNGCCG

(SEQ ID NO. 631)

## .....Rv68T7.seq:.....

CACGCGGTCTGGCCCGATCCGAAGATCCCTTTGCCGGCTGGCGGCTCTGCTCGGCGGTGTTGTACACTTCTCGAACA  
CCTCGGCACCGACACCAACCGTNGCTTGAACACCGCCAACATCGGCAGCAGATCTTGATGGTCTGGTGAATCCCA  
CGGTGACTTTGGAGTGGAAGGCGCCATACTGATCGCGCGCCAGCACATGAGCTAGCGGCAGGAAAACAGCAGCCGC  
TCACCTTGCGCAGCAGCGTCNGGTGATATGCCTGGCGCCCTTAATCTCGTGAACAGTTGGATTGGGTCAACTGGCAG  
CCTTGGGTCTCCGGTGGTGCCGANGTGTANATAAGCTCCCGGGTCCGTCAACGTANTGCGCAGGCGGCGGTTACTCGG  
CGGGTCAACGAGCCCCGCTCGTGAGCNATCAGCCTTTGGACCAGAACGGGATTCACTACCGCAGGCGGCCCTCCGAAA  
TCGGCACATGTCCTTTGATCGTTCGCAACAN (SEQ ID NO. 632)

## Clone Rv69

.....Rv69T7D3.seq:.....

GGCCATGTCACATCGGTGGTACAGGTAACCGCGCCGTGTGCGCGGTCTCGGAGATCAGAACGTGGTGGCAGTTGAAC  
CGCGGGCTTTTACGCCAGTCGCGATAATCGGCGGAAAGTCGGCGCCTGCCGCCCAACTAGCGCGACTCGCCACCTAGCA  
CACCGATGGCGAAGGCCATGTNTCCGGCCACGCCGCCGCGGTGCATACCAAGTCATCGACTAGGAAGCTAAGCGACA  
NCTTGTGACAGTGTTCGGGCAGTAGCTGCTCGGAAAATCGGTGGAACCGCATCAAATGGTTCGTTCCAATCGAACCG  
GTTACCCGATCGTCACAAAAATCTCCGTCTT (SEQ ID NO. 633)

## Clone Rv6

.....Rv6SP6.seq:.....

GGGTCTACAACCACCGGTCTGACTTCTGGGCTTCCACCGCTCGCGCCGTGCGGACAAACAGCGCGGTGGAACCGACA  
CTCGTTGTGATGTCCCAGCTATCACCTCCGGTAGGCACCAATCGACCCTACCCGGCTATCTACCCCCGATCTCCAG  
GCTCCGCCGATCCATGCGCATCCCGGTCCGGATCCC (SEQ ID NO. 634)

.....Rv6T7.seq:.....

CAGGCATGCAAGCTTGTGCTATTCCGTGGCACTGTGACACATATGCGCCGCTCCTCCTCATCGCTGCGCTCGGCATCG  
TCGCCGGCGGTTCATGGCGTCACCCTACCCAAGCCGAACGCGGAACGAGAACGTGTTCCATTATTAGGGTGTGAGCACC  
AATACCAGATTGCTCACCAGGAACTCACGCAGCACCGGGACGGATGTGAGCCACCACGCCATCTGGGGTGGTAGCGG  
GGAAATACGGCTAACCGCGCTCCGGTGCCGGCAGCCAGCGCAGACCCTCGGCGGCGGACACGGCTAACACGACGAC  
CCATAGTTGTTCTTTGCCGGATGGCCGTGTTTGCTGACATATCGGGCGCGGCGCGCGCGCGCCGCGCCGCGC

(SEQ ID NO. 635)

## Clone Rv70

.....Rv70SP6D2.seq:.....

NCTACGCTGCTGAATGTTGTGCGCCGAGGANTCAAGACCCACGCGGTGTACGCGGACNTGCGACATGTTCAACCG  
CCGGA (SEQ ID NO. 636)

.....Rv70T7D3.seq:.....

CTAACCAACAAGCCATGGTGGTTGGCGCCGTGAGAGGTGCGCGGTGCGCCACAACGGGAAGATCGCCTTGAGCGTCGC  
TCGACCGCCGCTCGAGTTGGGTGATAACGAAGTACTGATGCCGATCATGTGACGCTGTCCGTGCGATCAGCGTGCAG  
CGGCGACCCCTCGACGAGCCTCGGTGCCGCCGCGGCCAGGGCACCAGCTGTTTTAGCGCATTTGTGCTCCGCCCGGTAAT  
AAAGGANGTCGGTGCCTCCGCTGCTGTGTTGCGGAATAACATCTTCCCTTCTGCAACAGGATGAGAATGGTTTTA  
ATTGCTC (SEQ ID NO. 637)

## Clone Rv71

.....Rv71SP6.seq:.....

CTAAGCTTTCCGGTCCGCCGCCACTAGTACCGCGTTGCCGGCCCCGCCGACCTAGAATGTTCCGCCCATTTGCCGTTTC  
CTCCCGCCGCCGGGT (SEQ ID NO. 638)

.....Rv71T7.seq:.....  
TCTGGTGCCGGGTGTGCCGACGGGTCCGTCCGCCTCTGCTTCAGTGATTCTGTGATGCGACCGGCAACGTCCTCGTTG  
TTCGGTGTCTATGTGGTCCGTCTCTCCTTGTTCCGCATACGATT (SEQ ID NO. 639)

## Clone Rv72

.....Rv72SP6D2.seq:.....  
GCGATCGNTNACCACAAGGGCGCAACCGTTCCGCGCTCGACTGAACGTGCTGCCGCCTGGAGAACTGGCGCTGCTGCC  
ACCTGGTCCGCGCATCGGCACTTCGAGGACTGGATTTCGACGCGTGGCCCCGACCTGANGTNGGCGGTGGACNNGTGTG  
CACCCGGTTGATTCTCGGCCTTGCCGGGATGCCACCTGCGCCTGGTGGTCGAT (SEQ ID NO. 640)

.....Rv72T7D3.seq:.....  
CGTGACCGGACGGGGTGCCGCGCAACCGGTCTTGCCCAATTGCCGGGGACTGGGGCTGGAGTATAAAGCGGGCCTGT  
TGCCGGAAGATAAAGTCAAAGCGGTGACCGAGCTGAATCAACATGCGCCGCTGGCGATGGTGGTGACGGTATTAACG  
ACCGCCAGCGATGAAAGCTGCCGCCATCGGGATTGCAATGGGTAGCGGCACAGACTGGCGCTGGAAACCGCCGACGCA  
CATTAACCATAACCACCTGCGCGGCTGGTGCAAATGATTGAACTGGCACGNCCACTCACGCCAATATCCGCCAGAACA  
TCACTATTGCGCTGGG (SEQ ID NO. 641)

## Clone Rv73

.....Rv73SP6.seq:.....  
ATACTCAAGCTTCTTACCCANAGCATGAACCCCGCCGTCCAATGCCGCCACCGTGGTGTGCTGTCGGCCGGCCGGGTGCG  
GGCACAATCGCCGAGTTCGGCGAACAGATCCTCGAAGGTCTTCACGGCCAGCGATTGTTGCACGTGTGAGCCAGCCAA  
GTCACGGTGGTTTGACGCCACACGTTCCGCCACCGCCGCGCCGCGCATTAGGGCATCCTAATATAGGTTAGGCTACCCT  
ANTTATTCTGTGGTCNAAGGAGGCGAGCCGACGTGACCTTCCCGATGTGGTTCGCAGTTCGCCCGGAAGTGCCGTCA  
GCATGGCTGTCCACCGGCATGGGCCCCGGTCCGCTGCTGGCCGCGGCCAGGGCGTGGCACGCGCTGGCCGCGCAATAC  
ACCGAAATTGCAACGGAACCTCGCAAGCGTGTCTGCTGCGGTGCAGGCAACTCGTGGCAGGGGCCAGCGCCGACGGTT  
CGTCNTCCCATCAACCGTTCCGTATTGGCTAACCACCTGCACGGTGGCACCGCACAAACGCCGCCACAAACGCGCCCC  
GGTATAC (SEQ ID NO. 642)

.....Rv73T7.seq:.....  
GGCCGAACCTTAATCGGTTGTTGGCGGCTGCCGAGTTGGGTCACTCGGGGGGTGTGCACTGGCACATGGTGGGCCGGAT  
TCAACGCAACAAAGCCGGGTGCGTGGCTCGTGGGCGCACACCGCTCACTCGGTGGACAGCTCGCGGTTGGTGACCGC  
GCTGGATCGGGCGGTTGTTGCGGCGCTGGCCGAACACCGTCTGTGGCGAGCGGCTGCGGGTTTACGTCCAGGTGACGCT  
CGACGGTGCAGGATCCCGGGGCGGCGTGCACAGCACGACGCCCGGCGCCGTAGACCGGATTTGCGCGCAGGTGCAGGA  
GTGAGAGGGCTCGAACTGGTGGGTTGATGGGCATTCCGCCGCTGGATTGGGACCCGACGAAGCCTTTGACCGGCTG  
CAATCGGAGCACAAACGGGTGCGTGCATGTTCGCCACGCGATCGGTCTGTGCGGGCATGTCCAACAACCTTGAAT  
CCCGTCAACATGGTCGAC (SEQ ID NO. 643)

## Clone Rv74

.....Rv74SP6.seq:.....  
GCTTCCCTGATACTCGACCAGCCCCACTCGGGCCAATACGTGAATGTCCTAGCATTTTTACCCGTTACGGGCTAG  
TCGAGTAGTAGACGATTGATTAGCCTGAACGTACCTCCGACGGCCAGCTGACGAACGGGTTTGACGGA  
(SEQ ID NO. 644)

.....Rv74T7D3.seq:.....  
TCAGCTGTCTGTAGAAGGGCTGGCGATACTGTGCACTGTCTGATATCGCNNCGTNGTGGGACTATNCAGNCCATNANG  
ATGCGGTTTCNGNNNTGCAGAGNATCCTGGNACACATNCGGTTACGTTAATCANCATCGCGANTTCTNCGTNTTCG  
ATTANTTCTGCTAACGNNTCTNNNAGTGCTGCGGGTCGACTCTAGAG (SEQ ID NO. 645)

## Clone Rv75

.....Rv75SP6D2.seq:.....  
NCTCTGCCGGGCGNAGAGCGCAGAGTCGGACGGCTTCGTGCGATCGTGAAGCGACCNCGCATGANCAGATATCGNTNAC  
ACTGCTCANAAACTTCGGATCATCGNTGATACACAGGCCAACGGGTAGCGGTTGTCCAACCGCTTCGTCAACGANATG  
GGATCGTGACGANCTACGCTCGCAGGATATGTCGCNGACCNNTCTAGANAN (SEQ ID NO. 646)

.....Rv75T7D3.seq:.....  
CACTTCATGCTCGTGCCTTGGCNTCGATTGTCNCGAGNGGTTAGCTCCTCGAGTGNGTGACGTATCACTCCGGCNGAC  
TANCCGTATCNGCGTCCCGCACCGGTCAACTGGTCTAGCCACACGGGGAGAATNCNCGACCGGNGCTATCGACCNAT  
CACGGCTTGTGCNNAAGATAGNCAGCC (SEQ ID NO. 647)

## Clone Rv76

.....Rv76SP6.seq:.....  
ATACTCAAGCTTGCCAACCGCCACCCTGCATCCGGGGGGCGAGCACTGCTCCGCCGACCAGTACGAACCAACCTGCGG  
TGCCAGGCCATTGACAATGTGCTGGTCCGGCGCCCGGAGTTCTAGCACAGCAACGCCCGGCCACCACAGGGGCG  
(SEQ ID NO. 648)

.....Rv76T7.seq:.....  
CGGTGGGTGTGCTTGGCGGCGTCGGTATCAACACCGCCACGAAATGGGGCACAAGAAGGATTGCTGGAGCGGTGGC  
TGTCCAAGATCACCTCGCCAGACCTGCTACGGGCATTCTACATCGAGCACAACCGTGGCCATCAGTCCGGGTGT  
CCACACCGGAAGACCGGCGTCGGCGCGGTTCCGGCAAACCTTTGTGGGATTTCCCGCCCCC (SEQ ID NO. 649)

## Clone Rv77

.....Rv77SP6.seq:.....  
AATACTCAAGCTTCGCGGAGGTGGTGGGGCAGGAGCACGTCAACGCGCCGCTGTGGTGGCGCTGGATGCCGGCCGGA  
TCAACCACGCGTACCTGTTCTCTGGGCGCGTGGCTGCGGAAAGACGTGCTCAGCGCGTATCCTGGCGCGGTGCTTGA  
ACTGTGCGCAGGGCCCTACCGCAACCGTGCAGGGTCTGCGAATCCTGCGTTTCGTTGGCGCCCAACGCCCCGCGCA  
GCATCGACGTGGTAGAGCTGGATGCCGCCAGCCAGCGCGCGTGGAGCAACCCCGCGAGCTGCGGGACCGCC  
(SEQ ID NO. 650)

.....Rv77T7.seq:.....  
GATGGCACTCAGCTGGACAAGACCTTCACAAAATCTGAAATCCTGACCCGATACTTGAACCTGGTCTCGTTCGGCAA  
TAACCTGTTCCGGCGTGCAAGGACGCGGCGCAAACGTACTTCGGCATCAACGCGTCCGACCTGAAATGGCAGCAAACCG  
GCGCTGCTGGGCGGGCATGGTGCAATCCGAACAAGCACGCTCAACCCGTACACCAACCCCGAAGGGCCGCTGGCCCCG  
GCGGAACCTTGTCTCCA (SEQ ID NO. 651)

## Clone Rv78

.....Rv78SP6.seq:.....  
AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCTGGGCGTCTGGTGCCC  
GGCCTGCCGGTGCAAGAACTGGATTTTACTGCCATCTCTCGGACCCCTGAGGTGGTCCAGGCTTACAACACCGACCCA  
CTCGTGCAACACGGACGGGTTCCGGCCGGGATTGGCCGCGCGCTGCTGCANGTGGGCGAGACCATGCCCGGCGGANCA  
CCGGCATTGACCGCGCCGCTGCTAGTGCTGCACGGCACCGATGACCGGCTGATCCCCATCGAAGGCAGCCGTGCGCTG  
GTCNAATGTNTNGGATCNGCCGACGTGCANCTGAANGANTATCCCCGGCTGTNCCACNAGGTGTTCAACGAACCGGAN  
CGCAACCAAGTG (SEQ ID NO. 652)

.....Rv78T7.seq:.....  
CAAGGCATACGCCAAGACCCAAGGGATCGCAGTCACCTCCGTCAACGGCCTGGTCCGCCGGCCACGGGTCCGTGCAGGA  
GACGTGGCTGGCCATGCAAAGCGCCGCGCCTTATCAGGAACGCCCCGGCTTGTGCGCTTTTCTGTCATCGACACATT  
TCCGGAGGTGTTGTGGTTGGCGCANCGCGGAGACAGGCCTGGGATGGCGTGCATCGTATCGGGAATGCGATGGC  
AACACTGAAGTACGAGCGCATCCTGCGCCAGCATGACTGTTTCGACTACGTGCTGTTGGCGACGGGGANGTAGCGTT  
CACCAAGCTGGCCTTGGCCCTGGCGAATGACCTGCGGTTGACGACTCCCGGGACTAACCCGCCGTANTGAGCAAGGAC  
AGATTCTGCGCACACCCTCCTCGCTGGTGCACCTTGACA (SEQ ID NO. 653)

## Clone Rv79

.....Rv79SP6.seq:.....  
AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGCCGGTGATCTGGGTGGC  
CAACTCGGCGGGCACCATCTCCATCAGGACNGCAAACGCTCCGGCTTCGGCGACAGCGATCGCGTCTGCGATNGTTTG  
TTCGGCGGCGTCTCCGCGGCCCTGCACCCGGAAGCCGCCCAAGGTGTTGACNCTTTGCGGGGTGAAGCCGATGTGTGC  
CATCACCGGGATNCCCGCGCGGTGAGACANGCGATTGCTCGGCCACCGCTCACCGCCCTCGANCTTGACNGCATG  
TGCGCCGCGCTCCTTGAAGAAACCGGTGGCGGNGGCAACC (SEQ ID NO. 654)

.....Rv79T7.seq:.....  
CGTTGAGATCCAGCTGCGCACTGTGCAGCGCCTCGGTGGTCTGCTCGGCCGCGGATAACTCGTTGAGCTTGGCCA  
GCGCGTCTGCGCCGGATCAGCCAGCACATTGCGCGCCAGGACGCGCGAGGAGACGGTGAAGCTCGCAAAGAAACCTA  
TGGCGGACCGCATGATTACACGCGCGATCAACACCTCTGGTCGAGCCTCAAAATTTGCTTCTTAAACGGGCCATCG  
ACGGATGACGTGAGCTGGTTTAGGTCTCAAACAGGTTACGAAACGATCTCGGAATTGTCAAAGGGGAAGTTAAGA  
AAATGGATAGATTTCTACCATTTCGCTGTGGACGATCGTACTTCTGCTATAGGGCTCCAGGGGCATCGACACGCAACG  
ACCTTACGCGACACCGGATCCGCGTGGCGGCGGAACGGCACANGCGCAACCGAAGGGCCAATCCGACATCGG  
(SEQ ID NO. 655)



## Clone Rv7

.....Rv7SP6.seq:.....  
ATACTCAAGCTTATCTAGGCGCCAGCTTGATTGGTCTGGTTGCATTGGCCAGCTGCGCGAGCCTGGCTCACTTCAACT  
ACAACAACCGCAAACAATTGCCGCCTTCGGATCCGAGTTCGGTTGGGTACGCGGCAATGGANACCATTCTCGGTGA  
ATCAGACTATTCTTGAGTACTTGATCATCCACTCTGCACACGACCTGCGAACCCCGCGCGGCCTTGCCGACCTGGAGC  
AGCTGGCGCAACGTGTGAGCCANATCCAGGCGTTGCCATGGTTGCGGGTGTGACCCGGCCAAACGGGGAAACCTTG  
AACAGGCCCGGGCGACATACCAAGCCGGCCAAAGTTGGCAACCGGCTGGGCGGCGCGTCCGAATGATCGATGAGCGCA  
CCGGCGACCTGAATCGGCTGGCATCGGGTGCCAACCTGTTGGCCGACAATCTCGGTGACTTCGCGGTCAAGTCAGCCG  
GGCGTTGCGGGTGTCCGACGCTTGTCCAGCCCTCGCTTACTCCA (SEQ ID NO. 656)

.....Rv7T7.seq:.....  
CAGGCATGCAAGCTTTTTGAGCGTCGCGCGGGGCGAGCTTCGCGGCAATTCTACTAGCGAGAAGTCTGGCCCGATACG  
GATCTGACCGAAGTCGCTGCGGTGCAGCCACCTCATTTGGCGATGGCGCCGACGATGGCGCCTGGACCGATCTTGTG  
CCGCTTGCCGACGCGCGACGCGGTAGGTGGTCAAGTCCGGTCTACGCTTGGGCCTTTGCGGACGGTCCCGACGCTGGTC  
GCGGTTGCGCCGCGAAAGCGGCGGGTCGGGTGCCATCAGGAATGCCTCACCGCCGCGGCGACTGCACGGCCAGTGCCCG  
CGGCGATTTCAGCCATCGGGACATCATGCTCGCTTCATACTCCTCGACAGTCGGCGGAACAGCTCGATTCCCGGAACG  
CCCACGCATGGTG (SEQ ID NO. 657)

## Clone Rv80

.....Rv80SP6.seq:.....  
AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGTAGAAAAAGATCGGTGA  
GCGCATCGATTTCGCTCCGCCGGGTTTGCCGCTGCGGCGGCGGAGCTGCCGTGACCGTCTATTTGGGTGATCAGATACT  
GGGCTAGTTCGGTTCGGGTGGGGTGATCGAAGATCGCGGTGGCCGGCAGCGTTACTGCGGTGACAGCTGTTAAGCGGT  
TACGTATCTCCACGGCACTCAAGGAATTAAATCCCGAATCGGCAACGCCTGGCCAGCGTCNAGTCCGGCAGCGCCGT  
CNCGCCCCAGCACCGCTGCGGCATGCTCACATACCACCTCGATCGCTGCGGCGANTTGCTCGTCNGCCGACCGACCGG  
CCANCCGGGCGGCAAAACCNGAAGACCCAAGAATTATCACCACCATCGCTAGC (SEQ ID NO. 658)

.....Rv80T7.seq:.....  
CCTTCTTGACACCCACCTCGCCATCGACCTTGAGCACTCCGTCGTAGTTGGTGAACATGTGACCGGCGATCGGGCGGG  
TGAACCGGTACTGGGTGTGCGTGTGACGTTTATCTTACCACGCGGTAGCGCAGCGCTCCTCGATCTCCGACTTAA  
GCGAACCGAAGCCGCCGTGGAACACGAAATCNAACGGCTTGCGGTGCGCGGCAAGTCCGAGCTTGGCCGCGCCACCT  
GTTGCCCTTGCGCAAGGATGTGCGGGCGAANTTGACGTTGCGGGGCTTGANACGCCATGCACGTTGCCGAACGTGTCN  
CGGCCAGCANGTATTTGCCGTGCTCACCGGCGCCCANCGCCTCGATGGTTTTCTCGAAGTCTCCGGGCTGGTGTACA  
GCTTCTCGTTGATCTCGTTCGCCACGCGCTCTTTCGCCGCGGACG (SEQ ID NO. 659)

## Clone Rv81

.....Rv81SP6.seq:.....  
AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGGAAAGGAGATCCCCGGG  
AACCTGGTGGAACCCCGCCATTGGGGTTGTTGGGATGCGGATCAGCGTGAANGAAAGCTCGCTGGAGACAGCGGG  
TCGGCCGAAGCCGCAAGATTGGCCATCACTAGTGACGANATCGTGGCGCTCTGCGAGTANCCNAAGACAGTGACGTTG  
TTNCCGGCGGCAATTTGCTGCCGAATCGCACTTTCGAGAATGACNGCACCTGCGCCACCGANGAATCNAAGTGAGG  
TTCTTGATCAGCACCACCGGTTGAGCCCTTGGGGCGTGAAGANCGCCTGCGCNATAACACCCGGGACGCTGCCACTC  
ATGTNACGCGGTTTCGCGANCTCNACATATCT (SEQ ID NO. 660)

.....Rv81T7.seq:.....  
TCCTGGTGATCGANGGCCGCGGTTCCGGCCGAAAATCCGGTTCGGGTTTCGGGTCGCGGTTCCAACTTGANCGCGGTCC  
GCAGCTGATTACCGTGGAACGCGGCCAACTGCGCATAATGCGCATCCGAACCTCACC CGCCCGCCCGCGATCA  
CCCCAACCTGATCCAACGACAACCGCCCTCCCGCATACCCCGGGCGCAGCGCGGAACTCCGGCAACCGCGCGCCA  
CCGTGGCGATCGTGTGGCGTTGCTGACGAACANCCATCTTCCAGGCCACCAACCCCGCCACCGACCGCGCCCCG  
TCACACCCACAAACCGTCCGATCCAGCTCAGCCACGATCTCCACAATGCGCCCATCAATCGCATTGCGCTGAACGG  
GCAACTCCGCCAACTCCTCAA (SEQ ID NO. 661)

## Clone Rv82

.....Rv82SP6.seq:.....  
AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGATCTGGTACCCATCCGTGATA  
CATTGAGGCTGTTCCCTGGGGGTGTTACCTTCCACGAGCAAAACACGTAGCCCTTCAGAGCCAGATCCTGAGCAAG  
ATGAACGAAACTGAGGTTTTGTAACGCCACCTTTATGGGCGAGCAACCCGATCACCAGGTGGAAATAGGTCTTCAGC  
ACGTCGCAATCGCGTACCAACACATCAGCATATGATTAATTTGTTCAATTGTATAACCAACAGGTTGCTCAACCCG

TCCTCGAATTTCCATATCCGGGTGCGGTAGTCGCCCTGCTTTCTCGGCATCTCTGATAGCCTGAGAAGAAACCCCAAC  
TAAATCCGCTGCTTACCTATTCTCCAGCGCCGGGTATTTTCTCGCTTCCGGGCTGTCATCATTAAGTGTGCAA

(SEQ ID NO. 662)

Clone Rv83

.....Rv83SP6.seq:.....  
AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTANCGCCACCTCCCGGGCG  
GAACTCCACGGCGTGGATNAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGANGTCCGCGTT  
AGCGCCGGATTCCACCACATCCCTTGCAGAAANTCCGTTGGGTNCNATGATGTNCGCTTCTCCCNCTCNANATAATG  
GANCAACGCNATCCGTGCGGTACGGTTCCGGTCTNACTCCATGTNCGCGACCTTGGCGTTGANACCATCTTTGTATT  
GCGGCGAAAGTCNATCATCCGGTNAGCNCNATATGANCGCCGCTTTGTGCCGGGTGGTAATCCGGCCATGCGCNTT  
GCGTCCACCGCAACGTGCAACGGGGGNCNCAACGANNTTCTCCNGGGTTGAACCGGTNATCT

(SEQ ID NO. 663)

.....Rv83T7.seq:.....

TGTGTGTGGTGGTAACCATCTGAGCAGTGTGCCAACCGGGGCGAGCCAGCTCCCAATTGACGTGAGCCCGCTCACTT  
GCTGGGTAAGCGTCG

(SEQ ID NO. 664)

Clone Rv84

.....Rv84SP6.seq:.....  
AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATANAATACTCAAGCTTGCAGGTTNATNGCCTTGGT  
CAACGGCACCGTGATCGGATCNGGGTCTACCGCACACATNGACTGGAGCTTCCGGCAANTCATCGCTATGCCTCGCG  
GGGGGTGACGCTGANCCNCGGTGACNTGTTGNCCTCNGGCACGGTGCCACCTGCACGCTCNTCNACACCTCANGCC  
ACCGGAATCATTTCCNCGGTGGCTGCACGANAGCGANNTTGTCCNCTCCAAGTCTAAAGGCTGGGCGANANAAGCAN  
AACGTCCCGACNAACGGCACTCCTTTTCNNTTGTCTTC

(SEQ ID NO. 665)

.....Rv84T7.seq:.....

GAAATCATTGATGGTTTGAAGTACACAGGCCGATCAAGCCTTCGCCGAGCCAAATTCGAATCAAGAGGCCCAAGCCCGT  
ACCAATCAGCCCGGCAACGAGGGATTCCGTCAATATCAGCCAAATAACTGCTCTCGGGTTACACCCAAACAGCGCAA  
TATGGCGAAAAACGGTCGCGTTGCACGACATTAAATGTACGGTATTGTAGATTAAAAAGATACCCACCAACAANGC  
AATCAAATGAGAGCGGTTAAATTGACCGTAAAGCGTCCGTCACTCTGTTTGACNGTGTCCCGTTGGGTATCCGACGT  
TTCCATACGCACACCGGCCGCGAGTCTTTGTTGGATGCGTNTTGCAATGGCCTCATCTTTGATGATCAAATCGATGTN  
GCTCAGTCTTCCGGGCATATGGAACAACCTTTGGGCCGTGGAAATATCAGCAATGATA

(SEQ ID NO. 666)

Clone Rv85

.....Rv85SP6.seq:.....  
CTTTCGCCAGGCCGCGCGGATGTCCTCATCGCTTCACGAACATCATCCGAGCTTGACGCTGTCCCGAACAGATCC  
GCGCTGCCGCGCGCGCGGCCACACCGTTGCCGCGGATCGGCCCATCCCGAGGTGACCGCGCAGCTGGCTGGTCAGG  
CCGTCCGAGCTTTCCGGGAAGCTCGACATCGTCGTCAACAACGTTGGCGGCACCATGCCAACACGCTGCTAAGCACCT  
CGACCAANGACCTCGCGGACGCTTCGCCTTCAACGTGGGCACCGCCACGCGCTGACCGTCCGCGCGGTGCGGTTGA  
TGCTGGAACACTCCGGCGCGCGCAGCGTGATCAACATCAGCTCCACCATGGGCGCGGTGGCGCGCGGGGTTTC

(SEQ ID NO. 667)

.....Rv85T7.seq:.....

TGTGGGCTCCGATCCGGCGCGCATGGCATCGACGGCGACCGGATCGATGACGGCCAGGCTTACGAGCTTGAGGGTGT  
GAAGTTGTGGACCACCAACGGTGTGGTAGCGGACCTGCTAGTGGTTATGGCGCGGGTACCGCGCAGTGAAGGGCNCCG  
AGGGGGAATCANGCCTTTGTCGTGAGGCTGATTGCCCGGGATCACCGTGGAGCGGGCGCAACAAGTTCATGGGACT  
GCGTGGCATCGAAAACGGCGTGACCCGGCTTCNTCGCGTCAGGGTGCCCAAAGACAACCTTGATCGCANGGAAGCGACG  
GTCTGAAGATCGCGCTGACCACACTCAACGCCGGACGGTGTCCCTACCGGCGATCCAACCGGAGT

(SEQ ID NO. 668)

Clone Rv86

.....Rv86SP6.seq:.....  
GAGCTGGCCGAGCTGGACCGTTACCGCGGAACACTACGTTCTCGCTCGACGACTTTCAGCAGCGGGCTTGACGCGCG  
CTGGAACGCGGCCACGGTGTGCTGTGCGCGCCGACCGCGCTGGCAAGACAGTGGTCCGCGAGTTCCGCCGTGCAC  
CTGGCGCTGGCGGCCGGCAGTAAATGTTTCTACACCACGCCGTGAAAGCCCTGAGCAACCAAAAGCACACCGATCTC  
ACAGCAGCTACGGCCGTGACCAGATCTGGCTGCTGACCGGTGACCTGTGNGTCAACGGCAACCGCGGTGGTGGTGA  
TGACCACCGAAATGCTGCGCAACATGCTCTAC

(SEQ ID NO. 669)

.....Rv86T7.seq:.....  
GATCTCTGGATCGGCGGGGCTCTCCGGGCGGGCTCGGGGACCTCAGCGGGCGCGCCTTCCGGCCGAACCATTCCTT  
AGCCATAGATGACCGCACCTCGATGCACGGTTTGGCGGCAACGCGGCAAGGCGTCNGTCGGGCCCAGCCGCGGCAATG  
CGGGTACCCGGGAGCGCGGGTCNGTANACCANCGCTGGACTGCGTCGCGCGGTGCGTCNACNTCAAAGTCCCCGGCGT  
CCCATATCGCGTATGACGCGGGCGCGCCCGGCACCANGGGTGCCGATCCGGCCGTCTCGAACACCACCGGCCCGCCAG  
CCGCGCGGGTCCGGCAGCNAACCGCCCGCGCCGATACCCGCTGCCCGCGTGCCTGATTGACCGCCGCGCGCACGCT  
GGCCANGGATCAAAGCCCGTG (SEQ ID NO. 670)

## Clone Rv87

.....Rv87SP6.seq:.....  
GGACGCGTAGCCCGCCAGGCCGGTCAGGGTGCCCTTCCAGTCCACGCCGCTGTGGTGGCGGAACCGCTTATCTTCAAT  
CGAGACGATCGCCAGCTTCATCGTGTGGCGATCTTGTCCGAGGGCACCTCGAACCGGCGCTGCGAGTNCAGCCACGC  
GATCGTGTGGCCCTTCGCGTCGACCATCGTCGATACCGCAGGCACTTGCCCTCGAGCAGCTGGGCGGAGCCGTGGC  
AACGACCTCAGANGCAGATTGGACATCAGCCCTAGCCCGCTGCGAACGGGAACGTGAGCGCAGTGGCGACGACACT  
GGCCAACAGACAGCACCCAGCCAGCTTCAGAACGGTGATCGCGGCCGGGAAGCGCTCGGGCATGCGTNTACAGTAGC  
GACCTCCTGTCACTCCACGTGCCGCTCGGTCCAATAGAATCTTCCGCGGGCGGGTGAATCTCTGCNGGATCGGGGCN  
GGCGC (SEQ ID NO. 671)

.....Rv87T7.seq:.....  
GCTCGTTGCCGGCGCGATCTCGTCGAGCTCGTCTTCCATCGCCGCGGTGAAGTCGTAGTCGACGAGCCGACCGAAAT  
GCTGCTCGAGCAGACCGGTTACCGCGAACGCCACCCATGACGGCACCAAGTGCCTGCTTGTGACGTCNGCCGC  
GATCCTGGATGGTCTTGATGATCGACGANTAGGTGACGGGCGGGCGATGCCAGCTCCTCGAGCGCTTGACACGCG  
ACGCTCNGTGTNNCGGGCGCGGGTTGGTGGCATGGCCGTCTGGGGTCAACTCGACNATGTCCAACCGTTGACCCG  
GGGTCAGATGGGGCAGTCGCCGCTCGGCATCGTCAGCCTCGCCGC (SEQ ID NO. 672)

## Clone Rv88

.....Rv88SP6.seq:.....  
GTCTTTTCGATGGCTGCTTCTTCGGCGCTGACGCTGGCGATCTATCACCCCCAGCAGTTCGTCTACGCGGGAGCGATGT  
CGGGCCTGTTGGACCCCTCCAGGCGATGGGTCCACCTGATCGGCCTGGCGATGGGTGACGCTGGCGGCTACAAGG  
CCTCCGACATGTGGGGCCGAAGGAGGACCCGGCGTGCGACGCAACGACCCGCTGTTGAACGTCNNGAANTGATCG  
CCAACNACACCCNCGTCTGGGTGTACTGCGGCAACNGCAAGCCGTGCGATCTGGGTGGCAACAACCTGCCGGCCAAGT  
TCCTCGAGGGCTTCGTGCGGACCATCAACATCAAGTTCCAAGACGCCTACAACGCCNGTGGCGGCCACAACCGCGTGT  
TCGACTTCCCGG (SEQ ID NO. 673)

.....Rv88T7.seq:.....  
GCCAGGTCGAGGTCCCATGCGCGTGGGCCATTGATGCTGATCGCCAGGACGTCAAANATTTGGTCCGGCGTCAGCTGG  
GCGAAAAACGTGGGCCCGAGGACTTGCCCGGAGCTGCCCGGGTTCCCGTCGCGCAGCTCGGCGGGCCCGGTGAGAAAN  
AAATTGCGCCAGGTGCGACACTCCGCGCCGTANGCCAGCTGCTCCAGGGTGTGCGCATAGAGCCCGCGGGCCGAGCG  
TGCTCGCTGTGCGGCAACACCGCATGGTCGAGAAGCGTTGCCGCCCAACGGAATCACCTGCGTCNAANGCTTCGCGG  
GCCAATCCAGCACTCGGTGATG (SEQ ID NO. 674)

## Clone Rv89

.....Rv89SP6.seq:.....  
NAAACGTTCCGGCTTNGGTGCCGGGCGCTTATTTGCGTCTCTGGGATCACNCTCAGTCGCCGGCGGGTGGCGTTGGGC  
TATNANTTGACCGANCCGGAATCCGCACNANAACGTCNAGTAGCGGCCTGCAGAANTGCATCCTCGGCGAANCNG  
ACTACCGGTGGACANCAAGCGCCGCCGAACAACGCACTGGCCCGAGGGATNGGCGTCTATCGGCCCCGCGCGTGG  
AACTNGGAACAGACNGTGGGTTCTACCGTGATCTGGTGGGAATGCTCNACCANACCTTCCCNANNGCTACGGAACNA  
CGGCGCGATATTGCGCCTCCANCTCGAGCCTGACNCTNGATATCGTCGANNCTCACCATCNCGATCNGCTGTGCCG  
GTNTTGTCTCGGACTN (SEQ ID NO. 675)

.....Rv89T7.seq:.....  
CGAACGACGAACNCCNAAGCCATGGTGGTTGGCGCCGTCAAAGGTCCGCGGTGCGCACTACTGGAAAAATCGCCTTG  
AGCGTCNCTCGACCNCGCCCTCGAGTTGGGTGTCNTAACGAAATACCTGATGCCGATCANGTCNACGTTCCGTGCGNNG  
AACGTGACGCGCGACCCACTCTACNANGTCTCGGTNCCGCCNCGGCCAGNGCACCACAGTGACNAATCCNTGCGCC  
NTCGGGCCNAGCANTCCCGGTGCNACCGNGGTGGGTCCGGCGATGGTNGGGTGTNCTCNNTACNGGAACGCCAGCGCN  
ATCANCATCGGCANACTCNCGTGATGTGCCGCGGCGCAACCATCCCCACAATGATCNGGTGCGTCTGATCAGGCN  
(SEQ ID NO. 676)

## Clone Rv8

.....Rv8SP6D.seq.....  
TTAGGCGTGACGGCCACCGGGGCGCTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTC  
GCCGACTTTCCGCGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGC (SEQ ID NO. 677)

.....Rv8T7D4.seq.....  
CGTCACCCCGATGCGCCAGATCGGGGCTTCGCAGATAAAGCACGAAGTGGCGGGCAAAACGTCGATCTCGGAGCCGG  
AAGGGCAATCAGCCGACCGTCGACGAACGACACCGGCGAGACCACTTAGGCAGTGACGGCCT (SEQ ID NO. 678)

## Clone Rv90

.....Rv90SP6.seq.....  
CTTTTCNCGATGTCTCATGATNCCNANGGAGAACNNTGCNANCNCNGCCGCTGACNTNGCNCACCGCTNTGGCNGNGG  
TGACATTGGTGGTGGTTCGCGGCTGCNACGCCCCGACTCGANGCCGANCCATNTNTTGGCGCCGACCGCNTNTCGTCTC  
NACCGCANNCCCNATCTCNGCCGCNCCCGGTGGANCTACNGCTNCTTCGCCATCTCTCGCCNATGGCTCCNGCGNNTC  
GCNCAACGTNTGGTTGGTNANCTGCCTACCTGGTCNT (SEQ ID NO. 679)

.....Rv90T7.seq.....  
GCTGCGCCAGTCGTTCCGGTGCGGTCATGCCGTTGGACCNACCATCGGAGTTAGTTGCCGAACCGCGGACCACCGCAAG  
CACCCGGTCTGGTTCGCGCACCGCGTCGGCCAAACCGCTTGAGCACCACACGCGCGAGCCCTCGCCGCGCACGAATCC  
ATCCGCGTTGGCGTCNAANCTGTNGCATCGGTTCGGTGACAGCGCCGACCACTTGGACAGCGCGATGGCGGTGAA  
CGGTNANTAGGTGACCTGCCNCCNCGCCCCGCAATGCCACCTCCGCTTCACNCATGCGAATGGTCTGACACGCCNAG  
TGAATTGCCACCAGCGACAACAAAATCGGTATCTNCNGCGACGGCGGACACGCNATCCNACTGATACTCGATCCGC  
CCCACCGCTTGNANCTCCGGGTTCNGTGCTCATGTACCNCTCATGTCCGTCTGCGCNCGATATTGACGATCGTGTTC  
CCACGANNANAGANCCCTCATCACGCCGGTTCGAGTGCCG (SEQ ID NO. 680)

## Clone Rv91

.....Rv91SP6.seq.....  
CTGTGTGCGGNCGGCGCGATATCGGCCTTTTTACTAACCGAACCCGATGTGGGCTCCGATCCGGCGCGCATGGCATCT  
ACNGCGACGCCGATCGATGACGGCCAGGCTTACGAGCTTGAGGGTGTGAANTTGTGGACCNCCAACGGTGTGGTAGCG  
GACCTGCTANTGGTTATGGCGCGGGTACCGCGCAGTGAANGGCACCGAGGGGGAATCANCGCCCTTTGTCGTCTANGCT  
GATTCTCCCGGGATCACNTGGAGCGCNCNCNANTTCATGGGACTGCGTGGCATCCAANACGGCGTGACCGGCTTCA  
TCCNTCNGGGTGCCCAAAGACAACCTTGATCNGCNGGAAGCGACGTCTGAANATCGCGCTGATCNCACCTCAACGCCCG  
ACGCTGTCTTACCGCGGATCGCACCGGANTTGCCAANCCGCGCTNANNATNCGCGNGAATGNCCGTCCACNANTGCAT  
GG (SEQ ID NO. 681)

.....Rv91T7.seq.....  
TGGGGTGCCGGGCGCCGAGTTGCGTCCCTGGGATCACGCAGAGTCGCGGCGGGCTGCCGTTGGGGCTATGAATTGCACC  
GAGCCGGAATACTCCGANCAAACTGCGAGTAGCGGCTGCAGAAGTGCANCTCGGCGAAACGGAGTACGGTGGACA  
ACGAAAAGCGCGCGGACNACGCACTGGCCCCGAGGGATTGGCGTCAATCGGCCCCGCGCGTCAACTTGGGAAGANAC  
ANTGCGGTTCTACCGTGATCTGGTGGGAATGCTCCAACNNACCTTCNCCGAAAGCTACGGAAGCNACGGCGCGATNTT  
CGGCCTTCCAGCTCGACCTGACGCTGGAATCG (SEQ ID NO. 682)

## Clone Rv92

.....Rv92SP6.seq.....  
NGGCNNGGAAGTTAATGCCCTACTGGTTCNATGCTCNACNTCNCNGTGACNNCCTGCNCCGACCCGCCGAGGTCCCT  
GNCCGTNACCACCGANCNGGCGATCCGGGACTCTNGTACGCATCCAACANNGANCAACGTGCACGGGCGGAGTNGTNC  
CGCCACTTCGNATGACGGGGTCGATCCNTTCGACGTCGCTCGCCGCGTCCGTGAGTGGCGGTCACTCCNNGTA  
CTCGACCNCACNGACGAGGACTCGANCCCATCTACGTGTGGACGAAACANATCTTCTGTCCNACGACTACACCACC  
ACCCAGGCCATCGCCGNCGCCCGCGANGCCCTTCGACGCCNTACTGGTCCNGNGGNGGCGCTCTCCGGTGTCTNNC  
NCNTGNCGTGTTCTTACNCACTGCCNACATCGANCCGAGCNATNCNANGTCCGTCAATC (SEQ ID NO. 683)

.....Rv92T7.seq.....  
GGACACTGTTTCGCTGCCCTCGTCAAAGCCGGAGTGGTCTGCTGCGCCGGACCCGACCCGACCTTCAGCGGGGGTT  
CACAGCTCCGTGGGTGCCGTTACTTCCGATCGCCGAGTGTGCGCGTGCCTGTGGCTGATGCTGAACCTCACCGCGTT  
GACTTGGATCCGTTCCGGATCTGGCTGGTGGCCGGAACCGCGATTTATGTGNGCTACGGGCGCCGGCACTCGGCGCA  
TGGCCTTCGGCAAGCNCNANANAACGCGACCCGGAGGTGTTGAAGTAGCTTCGCCGCGTATTACAAATTGCNTTATA  
TGTCTACACATAAGACGCAAACTGCTCTATTGTCAANTCCANCCTGGTGTGGCNCATGAAGATGTTTG (SEQ ID NO. 684)

## Clone Rv94

:Rv94SP6.seq:::

TCCTTCTCGGTATCGGTTTGGGCTGTACCCANCAAGTTGGTAGTTCTTCACGTNCTGTTGTTTCGAGCGTCNAGCCGTCG  
CGCGTGTCTNANGTCNCCGGACGCGTATCCCGCCAGGCCGGTCANGGTGCCCTTCCANTCCACGCCGCTGTGGTCGGCG  
AACGCTNATCTTCAATCGAGACCATCGCCAGCTTCATCNTGTTGGCGATCTTGTCTNACGGCACCTCNAACCGGCGCT  
NCTAGTACNCCACNCNATCNTGTTNCCTTCNCGTCNACATCCTCGATNCCNCTGCACTTTCCTCGANCNCCTGGGC  
CGAGCCGTTGGCANTNACCTCNGAGCCCCATTGGACATCANCCCCANCCGCTGCGAACGGGAACGTCAGCNCNCTGG  
CGACAACCTGGCCAACAN

(SEQ ID NO. 685)

:Rv94T7.seq:::

CACNCCGTGATCGCNAGCCCCNGTAGAAATNGTTGAGCCAGTTGGTGCGGCGCTCGTTGCCGGCGGTNATCTCGTCTGA  
GCTCNTCTTCCATCGCCGCGGTGAAGTCGTACTCGACNAGCCGACCNAATGCTGCTNAGCAGACCGGTTACCNNA  
ACNCCNCTCNTGACNGCACCAGTGCNCTGCCCTTCTTGTGCACGTACCCGCNATCCTGGATGGTCTTGATGATCNAC  
TANTNTGTGACGGGCGGCGGATGCCATCTCCTCNAGCGCTTTGACCAGCGACNCCCTCGGTGTATCGGGCCGGCGGG  
TTNGTGGCATGGCCGTCTGGGGTCANCTCNACNATNTTCANCCGTTGACCCGGGGTCACA

(SEQ ID NO. 686)

## Clone Rv95

:Rv95SP6.seq:::

TGGCCTTCTTGNCANGGGCNNACATNNGCTATNGCGAGCGTGTAACCGATCATCNTCCNGGCGACTGTGGCCTGANCG  
GCAAGGGTNGCCTNATTCTCTCTGNGGCATGGTTNCCACACGGAATGNCGGTAAGTCTGGTTCGGCAACCTGGCCC  
GCTGCGGGTTGGGTTTCGGATTTCGCTCGGCTANTAAAGGTGCTCGCCTGGTGTNACNACTAATCNATATACNCTTANC  
GGGAGTNGNCGTCCCGATCTTNGCCCTGCCGCGNGGCGATCNCGTTTCGCANACCCGCCACCGGAACCTCNAANGTCCGC  
TCATCGGGCTCTACGCGCCATCTTCCCGGATTCTTTCGCGGCGNGGTNCCGNGGGACCCCGGACTGTGACNGGCCCAA  
CGGCTCATCATCG

(SEQ ID NO. 687)

:Rv95T7.seq:::

CCGGATAGCGGTGTCTGAAGTTCCCGCTTCCCTCCANCGCATTGAGCTTCAGCCCGACCGGCAGGTNNGGAGTCGGC  
ATGCGGTCTCTCGCCCCGACCCCGCTGGCTAAATANCCACCCCGAGCGCGGTACAGGTCTTTGCACCGGGACGACGC  
ATACCGGCAGCGCGAACATCNCGCGGGGCTGCAGCNTGAACGTCCAATACCANTCNAACAGTGTCCGCGCGTNAACAC  
CCGANCCGGCGGTTCGCTTCNGTAATCAACGGCTCCTGCGCAACAGTGCAAGTTCGCGGTGCCACCGGCGTTGACGA  
TCTTGATGTCTGCGANCTCGCGCACCCAGCTCGACGGCCCGGCA

(SEQ ID NO. 688)

## Clone Rv96

:Rv96SP6.seq:::

CCTCCCGACCACATACAGGCAAAGTAATGGCATTACCGCGAGCCATTACTCCTACGCGCGCAATTAACGAATCCACCA  
TCGGGGCAGCTGGTGTGATAACGAAGTATCTTCAACCGGTTGAGTATTGAGCGTATGTTTTGGAATAACAGGCGCAC  
GCTTCATTATCTAATCTCCAGCGTGGTTTAAATCAGACGATCGAAAATTCATTGCGAGACAGGTTCCCAAATAGAAAG  
AGCATTTCTCCAGGCACCAAGTTGAAGAGCGTTGATCAATGGCCTGTTCAAAAACAGTTCTCATCCGGATCTGACCTTT  
ACCAACTTCATCCGTTTTCAGGTACAACATTTTTTAGAACCATGCTTCCCGAGGCATCCCGAATTTGCTCCTCCATCCA  
CGGGGACTGAGAGCCATTACTATTGCTGTATTTGGTAAGCAAAATACGT

(SEQ ID NO. 689)

## Clone Rv9

:Rv9SP6.seq:::

CTTCACNTCCGTACGGCTCGGGTACGCTTCGGTCNCATTGTGCGAGTGATAGATGACGACCGGGACCTCGTCGGCATC  
TTCCATAGCCCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGGTANAAGGTGGCGGANCCTCNGCATTGGTCAT  
CGGGATATGCCGCTCGGGACGGTCANAGCCCTCGGGTCCGGCCAGCACTCCGCAAGGCTTCGTGGGGGTGGTTCGCGACG  
CGCATGGGCCACCATCGCATTACCAAGGTCTGCGCGAATCACCAGCACGTANACGGTTCTTTCTAAGCAACACCGA  
ANTTTAGGACCCGAATGCTCCGGGAAACATGTACGGTAGGTTCGGTATTCGGCTACCGGCTGANCATTGAGCACGC  
CGGCCAGCACCGCACGAACAGGCAATCAGCCGCCGCCGACCCGACCGCG

(SEQ ID NO. 690)

:Rv9T7.seq:::

CAGGCATGCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACCACGCGCGGGTTCGGGCGCCGGGCC  
CGGGCCCGCAGGTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCGGCTGCGCTACGTGAGCCATACCGG  
GCGGAGCTACATCGGCTCGGCCGCCAGTGTTTCGGGCCCTTTTCGAGGTTCGAGGTTCGATACCGATTTCGCGCATCCGC  
AGCCGCACCCTGGACGACAGAACCGTGCCCTACGAATTGCTTGTGCGGCGGGGCCAAAGAACAGCTTGGCATCTGGC  
GCGATTGGCCGGCGCGGCGCTGGTCGCCAAGGAAGACCCGTTCCGGTGTGAT

(SEQ ID NO. 691)

Table 4 : End-sequences of the polynucleotide inserts cloned in the named recombinant BAC vectors contained in the I-XXXX *M. bovis* strain Pasteur genomic DNA library.

RvXXXSP6 corresponds to the SP6 end-sequence of the clone RvXXX.

RvXXXT7 corresponds to the T7 end-sequence of the clone RvXXX.

RvXXXIS 1081 corresponds to a region located close to a copy of the IS1081 repetitive sequence (Insertion element).

The character « - » denotes an uncertain base residue.

#### Clone X0001

.....X0001SP6.seq:.....

AAG-

TCGGGTTTCCACACGCGCGGTTTGACCCTAGTCATATGTAATCATGTGTACCATGTGCGGGCGCTTTTCGACGGCCG  
CGAACCACCGGA-ATTTCTGTGATTTCACTGCATGCGTACCATCTGGCACAATTGAGCA-TTGTCT-  
TCGCGGTGGTTCGG-CGGGTTGCGTGCCGCCTGCTGCGA-ATGCACCA-  
TAAGCCCGAACCCACCGGCTTGGTGACCACCGCAGCTGCGTGTGGGGGGTAACCACTCCGCGACCCCAAGGATGGT  
CATTTCCAATGAACCGGCTGGACTTCGTCCA-A (SEQ ID NO. 692)

.....X0001T7.seq:.....

GTCGCGGTTTCGATCGACCCGATCTTCACCTCGTAACCTCGATGCTTAGCAGGATCCAGCTTGACCGCGTTTGGCTCT  
ACCCACTCTTTGAGTGGCGCCGTCGCCTGTGCCCCATCGGTGTTTCATGACGAACGCTTCGAAAGACTTCCTCTTG  
AGCCGGAATGTCTGCGTAAAGAAGTTCATGTCCGGGAAGTAGACCCGGTTCGCCCTCCACGTGGTACTCCTTCGAGG  
TCCGCTTCTCGCCGGATCCGATAAACACCGGCCCCAGGCACCGCAGCGTGAGTTCGAACGGCTTCAGGTAGGTGTTT  
ATGCGGCGGACTCCGGGAGTGCGAGAAATAGCGGTGCGCGTAGCTGTAGACCGGATGGTTTCCGCCCCAGGCTGACG  
TCGAAGATGCCTCCTTGGAAGGGGCGCGA (SEQ ID NO. 693)

#### Clone X0002

.....X0002SP6.seq:.....

AACTCAAGTTTTTACGGTGATCGCGCATCACCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCA  
ACATGAGCCAGCCTCTCGTCGGCGGTCGGGTGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCCTGACCCTGAAA  
CCAGCTTCCATATCCCGCGAC-  
AACGACGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTTCTCCACCGACCGGGCCCGG  
TGT (SEQ ID NO. 694)

.....X0002T7.seq:.....

GTGCAGGTTTCGACAAATGGTGCCGGTTCGGCGGCTACGTGCCATCGAGACACTGGCGCA-GCTATCGCACCCGTT  
ATCGGCTGCGAGCAAATCGCGGTATGCGTTCTTGAGCATGAGTCGGCGACCGTCGTATGGTCGACACCCACGACGG  
AAAGACGCAGATCGCCGTCAAGCATGTGTGCCGCGGATTATCAGGACTGACCTCCTGGCTGACCGGCATGTTTGGTC  
GCGATGCCTGGCGCCCGGCCGCGTGGTTCGTGGTTCGGATAGCGAGGTGAGCGAATTCTCGTGGCAGCTCGAA  
AGGGTCTGCCGGTGCCGGT (SEQ ID NO. 695)

#### Clone X0003

.....X0003SP6.seq:.....

TTTCAGTCATGCGCCCGCCTCGACCACGAA-ATGCACGTG-  
GGTTCGATCGACCCGATCTTCACCTCGTAACCTCGATGCTTAGCAGGATCCAGCTTGACCGCGTTTGGCTCTACCCA  
CTCTTTGAGTGGCGCCGTCGCCTGTGCCCCATCGGTGTTTCATGACGAACGCTTCGAAAGACTTCCTCTTGAGCCG  
GAATGTCTGCGTAAAGAAGTTCATGTCCGGGAAGTAGACCCGGTTCGCCCTCCACGTGGTACTCCTTCGAGGTCCGC  
TTCTC (SEQ ID NO. 696)

.....:X0003T7.seq:.....  
GTCATGTGTACCATTTGCGGGCGCTTTTCGACGGCCGCGAAACACCGGAGATTTCTGTGATTTCACTGCATGCGTA  
CCGTCTGGCACAATTGAGCAGTTGTCTGTGCGGGTGGTGGCCGGGTGCGTGCCGCTGCTGCGAGATGCACCAAT  
AAGCCCGAACCACCGGCTTGGTGACCACCGCACGCTGCGTGTGGGGGTAACCACGCCGCGACCCCAAGGATGGTC  
ATTTCCAATGAACCGGCTGGACTTC-TCAACAA (SEQ ID NO. 697)

## Clone X0004

.....:X0004T7.seq:.....  
AACAGCGCGGTTGAACTGATAGGTGCGGCCGGCTCGAGCAGGCCGGGCCATTTGTTTCGATGCGGTTACCGAAAGAT  
CTCTTCGGTGACCTGCCCGCCGCGCCAGCTCGGCCAGTGCCCGGCGTTGGCCGCCGCGGCGACGATCTTGCGCT  
CCACGGTGGTCGGGG (SEQ ID NO. 698)

## Clone X0006

.....:X0006T7.seq:.....  
GCATCTGGGCTGGCGGTGGTTCGCGGCTCCGAAGCCGTGGAACACCATCGCCAGCGGGCTTCCACATCAACGACCA  
TTTCGGCCAGCTTGCGGCGCATCAGCGGCTTGTGATGAGCGCCCCACCGAATGCCCGCCGCTGCCCGGCGTA-  
CACAGCGATTGACACAGCGCGCGCGCGCTTGCCGAGGGCGAACGAAGCGGTGCCCAACCGCAATCTGTTGGTCAG  
CTCCATCATGCGGGTGAGTCCCTTGCCG (SEQ ID NO. 699)

## Clone X0007

.....:X0007SP6.seq:.....  
ATCGGTTTCCAGCAACAGCCGATCGACGGCTTCGCCCA-  
GGCCGCTCCCGGGCGACCCGACCATTTGCTGTCGCGCGTAACGCCATCACGGATGACGCGCAGTTCGTGCTGTCTA  
GCTCCACCATCGCCTGCACACCGGCGGCCAG-ACCCATTGGCCGTGCGACTCGTA-  
AGCAGGTAATCCTCGTCGACGGACTCGGTAACCAACCGCCGCGCAGCTCCGCTGCCAGGTGCGCGGGGTTGACACCGGC  
GGGCATCGGGATGGACGACGACGCGGTGCTGACGGCGCCTGTC (SEQ ID NO. 700)

.....:X0007T7.seq:.....

AGCGGTTTCCCA-  
GCGGGATGTGCTGTGAGCGCCGCACCACCAGCGCCGACGCTAAGGATGGAACGCACGGCATCTTCTGACGCGTAACC  
GCGTTGTGATCGCGAGCTGAGGAGACGGTATGGGGGAGGGTTCTCGGAGGCCATCTGGGATGTTGATGTCTGTGAT  
CTTGAGCCCGGTGCAACTCGTCGGCCCGGACGGTACGCCGACGGCCGAACGCCGCTACCACCGTGACCTTCCTGAGGA  
AACGCTGCGTTGGCTCTACGAGATGATGGTGGTCAACCGCGAGCTGGATACCGAATTCGTCAATCTGCACG

(SEQ ID NO. 701)

## Clone X0008

.....:X0008SP6.seq:.....  
CAAGCTTCCACAGGTAGGGATCGAGGAACAGCGGTTGAACTGATAGGTGCGGCCGGCTCGAGCAGGCCGGCCATT  
TGTTGATGCGGTTACCGAAAATCTCTTCGGTGACCTGCCCGCCGCGGCCAGCTCGGCCAGTGCCCGGCGTTGGC  
CGCCGCGGCAACGATCTTGGCGTCCACGGTGGTGGGGTCATGCCCGCGAGCAGGATCGGCGAGCGGCCGGTACGCC  
GGGTGAACCTTCGTGAAAGCTTGACCCTGCCGTGCGGGAGGCGAACCACGGTCGGTGCGTANCTCCACCAAGCCCGG  
GCAACCTCGGGGGTGGCGCC (SEQ ID NO. 702)

.....:X0008T7.seq:.....

TGGACCTCATGACAACGCGGCGCGGATTACCCCGCTACCGCCAGCAGCATGACGGCGGTAGCGAACACCGCCGGAT  
GCAGCGCAGGTGCGTCGATGTGCTCACGGAATCGCCCCGGCACCGCGATCTCGAGGATCACAGTGCCACCCCTGC  
AGCGCGACACCGACGATTCCGTACACCGCCACGCCGATCAGGCCCTGGGCCAGCTGGCGTATATGGCGGCGATGGTG  
ACGATGGCCAGCGCCACATACATTGTGGCGGCCAGAACCACGGCGTTGGGGCGGCGGTGATGAACACTAGGCGACG  
CAGATCGCCCGGGTCAACAGGTTGACCATCAGAAAGCCTGCGA (SEQ ID NO. 703)

## Clone X0009

.....:X0009SP6.seq:.....

TTTGGTGCGGCCGGCAATCAACTTC-GCTC-  
CAGCGGTTTCCAGCGGGATGTGCTGTGAGCGCCGCACCACCAGCGCCGACGCTAAGGATGGAACGCACGGCATCT  
TCTGACGCGTAACCGGTTGTGATCGCGAGCTGAGGAGACGGTATGGGGGAGGGTTCTCGGAGGCCATCTGGGATGT  
TGATGTCTGTGATCTTGAGCCGGTGCAACTCGTCGGCCCGGACGGTACGCCGACGGCCGAACGCCGCTACCACCGT  
GACCTTCCTGAGGAAACGCTGCGTTGGCTCTACGATATGATGGTGGTCACCCG (SEQ ID NO. 704)

.....X0009T7.seq:.....  
CGCCCAGGGCCGCTCCCGGGCGACCCGACCATTTGCTGTGCGCCGTAACGCCATCACGGATGACGCGCAGTTCGTCTG  
CTGTCTAGCTCCACCATCGCCTGCACACCGGCGGCCAGGACCCATTGGCCGTCGCACTCGTAGAGCAGGTAATCCTC  
GTCGACGGACTCGGTAACCACCGCCGCCAGCTCCGCTGCCAGGTCGGCGGGGTTGACACCGGCGGGCATCGGGATGG  
ACGACGACGCGGTGCTGACGGCGCCTGTCGCGACGCTGAGCTCGGACACAGCTAGTAAATGTAGCCTAACCTACTTA  
ATGGGTGCGAGCCCCCGGGTCGTGCGATGTCCAACGTTGCTCGACTGGAAGAAAATGCTCGTCGGGGAGCAAATG  
GCACC (SEQ ID NO. 705)

Clone X0010  
.....X0010SP6.seq:.....  
AATACTCAATCTTGATCGGTTTCCAGCAACAGCCGATCGACGGCTTCGCCCAGGGCCGCTCCCGGGCGACCCGACCA  
TTGCTGTGCGCCGCTAACGCCATCACGGATGACGCGCAGTTCGTGCTGTCTAGCTCCACCATCGCCTGCACACCGG  
CGGCCAGGACCCATTGGCCGTCGCACTCGTAGAGCAGGTAATCCTCGTCGACGGACTCGGTAACCACCGCCGCCAGC  
TCCGCTGCCAGGTCGGCGGGGTTGACACCGGCGGGCATCGGGATGGACGACGACGCGGTGCTGACGGCGCCTGTCGC  
GACTCTGAGCTCGG (SEQ ID NO. 706)

.....X0010T7.seq:.....  
GGATGTGCTGTGAGCGCCGACCAACAGCGCCGACGCTAAGGATGGAACGCACGGCATCTTCTGACGCGTAACCGCG  
TTGTGATCGCGAGCTGAGGAGACGGTATGGGGGAGGGTTCTCGGAGGCCATCTGGGATGTTGATGTCTGTCGATCTT  
GAGCCGGTGCAACTCGTCGGCCCGGACGGTACGCCGACGGCCGAACGCGCTACCACCGTGACCTTCCTGAGGAAAC  
GCTGCGTTGGCTCTACGAGATGATGGTGGTCACCCGCGAGCTGGATAACGAATTCGTCAATCTGCAGCGCCAGGGGG  
AAGCTGGCGTTGTACACGCCCTGTCGCGGGCAGGAAGCCGCGCAGGTGGGTGCGGCGGCTTGCCCTACGCAAAACCGA  
CTGGTTGTTCCCC (SEQ ID NO. 707)

Clone X0012  
.....X0012SP6.seq:.....  
ATCACGACAACAGCGACGGTGTGTCGGATCAGCGCCCCCGTTGCCGGGCAATGTTGAGGCGTTTCTGCGTCTGGTT  
GAGGCCGGCTGGGAC-  
CCGAGGTGGCTCGTCGGCCACATGGGCAGCACACCACCGTGATGCATCTAGACGTGCAGGACCGTGCCGCTGGC  
CTGCA (SEQ ID NO. 708)

.....X0012T7.seq:.....  
GCGGCTACGTGCCATCGAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTGCGAGCAAATCGCGGTATGCGTTC  
TTGAGCATGAGTCGGCGACCGTCTGTCATGGTCGACACCCACGACGGAAGACGCAGATCGCCGTCAAGCATGTGTGC  
CGCGGATTATCAGGACTGACCTCCTGGCTGACCGGCATGTTTGGTCGCGATGCCTG: (SEQ ID NO. 709)

Clone X00013  
.....X0013T7.seq:.....  
TACAAGCGGCACCTCGCCGGTGAAC TGACCGTTTCGCACGCTGCGCACCGCCGCCGGGCGCGTGCTCGGCGCGCCGGC  
GGCCCCCGAGGCGCTGAGAGGGGAACCAACCATGCAGGTGAACATGACGGTAAACGGCGAGCCCGTCAACCGCCGAGGT  
CGAACCCCGGATGCTGCTGGTCCATTTCTCCGTGATCAGCTGCGGCTCACCAGGAAC TACTGGGGCTGTGATACCA  
GCAACTGCGGGACATGCGTGGTGGAGGTCGACGGCGTGCCGGTGAAATCCTGCACGATGCTCGCCGTGATGGCCTCC  
GGGC (SEQ ID NO. 710)

Clone X0014  
.....X0014T7.seq:.....  
AGCGGCTGGTTACGACTCCCTGTTTGTGATGGACCACTTCTACCAACTGCCCATGTTGGGGACGCCCCG-CC-  
TCCGATGCTGGAAGCCTACACTGCCCTTGGTGCGCTGGCC-C-GCGACCGAGCGGCTGCAACTGGGCGC-  
TTGGTGACC-GCAATACCTACCGCACCCC-ACCCTGCTGG-CAAA-  
ATCATCACACGCTCGACTTGGTTAGCGCCGGTCGA-CGATCCTCGGCATTGGAACCGGTTGGTTT-  
(SEQ ID NO. 711)

Clone X0015  
.....X0015SP6.seq:.....  
ACGCGCGCCGATCATATCTGCTATGGATGTACAATTGAGCTCTTGCTGTTATACCACTATATGGTGTACTATTTGAT  
CTATGCTGACGTGTGAGATGCGGGAATCGGCCCTGGCTCGACTCGGCCGGGCTCTGGCTGATCCGACGCGGTGCCGG  
ATTCTGGTGGCGTTGCTGGATGGCGTTTGCTATCCCGGCCAGCTAGCTGCGCACCTCGGGTTGACCCGATCGAATGT  
GTCCAACCATCTGTCGTGTTGCGGGGCTGCGGGCTGGTA-TCCCAACCTATGAGGGCCGGCAGGTTCCGGTAT  
(SEQ ID NO. 712)



.....X0015T7.seq:.....  
CCGCGCTGCTGCTGACGTGCGTGAACGTGCGACACGTCTGCGAATACCGGCCGAACGCTGGGTTTATCCACAGGCT  
GGCACCAGACGCCACGACACACCGGCCGTGCGCGACCGCCACCGACTGCATCGGTGACGCCATTTCGGATCGCCGG  
TGCCCGGGCGCTGGAAGTGGCTGGGCTGGGGCTCGATGACATCGAATACGTGACCTGTATTTCGTGCTTTCCCTCCG  
CTGTCCAAGTCGCCGCAATCGAATCGGCCTGGACACCGACGATCCTGCCCGCCCGTGACCGTCACCGGGGGCCTG  
ACCTTCGCCGGCGGGCCGTGGAGCAATTACGTCACGCACTCCAT (SEQ ID NO. 713)

## Clone X0016

.....X0016SP6.seq:.....  
CAGGCGTGCAATGACCTGCACTGCGCCGGA-A-  
TCCCTAACCCACTAAACCGGGGCCGCTCACAAGCCGTGCGAGTTCGGTCAGCGTCAGGTGCGCGACCAGGAA-  
TAAATGAGCAGACCGGTGCGGTCAACGATGGTGGCGATCATCGGCCCGGAAACGATGGCCGGGTC-  
ATGCGCAACTTCTTCAGCAGCGCGGAAGGACGGCA-CCACCAGCGAC-ACCACACCAGAT (SEQ ID NO. 714)

.....X0016T7.seq:.....  
GCGAA-  
CACTTCGTCAACTTCCAGGGCTGCCCCGACCAAGTATTTTCGACGAGTATTTCCGTGCGGCCGCCGCCGCCGCCGCCGCGC  
GGCAGGTGGTCATCCTGGCGCGGGGCTGGACTCGCGCGCGTACCGGCTGCCTTGGCCCCGACGGGACCACGGTTTTT  
GAGCTGGACCGCCCGCAGTTCCTTGATTTCAGCGCGAGGTGCTCGCCAGCCACGGTGCCCAACCGCGCGCCCTGCG  
CCGCGAGATCGCCGTGACCTGCGTGACGATTGGCCACAAGCCTTGCGGGACAGTGTTTCGATGCGGCTGCACCGT  
CGGCATGGATTGCCGAAGGGCT (SEQ ID NO. 715)

## Clone X0017

.....X0017SP6.seq:.....  
TTGGGC-TTGCCC-CAATA-GGCCCCAATCAAAGCCGAGCAGGTGGAACCTA-CGCATTGCCTC-TCGT-  
TGTGCACCCGAGCCATCGCACGCGCGGGAATTCCCGGAT-TC-  
CCGTATTCTCCGGCGGCCGGGCTAACCCATCCCA-GCCGAACGGTTGGCTC-  
TGCCGTGGGTCCCGTGTGGCCGATCGGGGCGTCACCGGGGGTGCTCGGGTGCGG-TGACCATGGC-AACTGCCCC-  
ATGGGCCGACCCTGGTGCAGATAAACCTG (SEQ ID NO. 716)

.....X0017T7.seq:.....  
TGGTGGAGGTCCCCACCAA-ACCGGCCGTAACTCTGCTACGGAAATGCGG-  
CAGGCCGCGCTAGCACGTGGTATCCGCCATAAAGGTGCACCTTAAGCACGGCGTCCCAATTCTCGAACGACATCTT  
GTGGAAGGTGCCGTGCGCAAGATCCCGCGTTGCTCACCACACCGTGCACGGCGCCGAATTTCGTCAAGCGCGGTCT  
TGATGATGTTTCGTGCGCCGTCTCGGTGGCGACGCTGTTCGGTA-  
TTGGCGACCGCCCGCCCCCTTGTGCGGAAATCTCGGCGACGACCTCATCGGCCATCGCCGAACCGGGCGCCCCG  
(SEQ ID NO. 717)

## Clone X0018

.....X0018SP6.seq:.....  
GCCGGCCAACTGGCCGGCGGGTTGCTGTC-TCAAGGTGGGTTCCGCCACCAA-ACC-  
CACTCAAGGATCGCAAGGAAAGC-  
TCAAGGATGCGGTGCGGCGCCGCAAGGCCGCGGTCAAGGAGGGCATCGTCCCTGGTGGGGGA-  
CCTCCCTCATCCACGAGCCGCAAGGCGGTGACCGAACTGC-TGCGTC-C-GACCGGTGACAA-  
GTCCTCGGTGTCCACGTGT-CTCCGAAGCCCTTGCCGCTCCGTGTTCTGGATC-CC-CCAAC-  
CTGGCTTGGACGGCTC-GTGGTGGTCAACAAGGTGAGCGAGCTACCGCCGGGCATGGGCTGAACGTGA  
(SEQ ID NO. 718)

## Clone X0018

.....X0018T7.seq:.....  
CGAACCT-AATTGTCCTGTAATGCCAGCTCACCAA-  
GCATGGCTGGTGGCCGGGCGGTGAAGCCGGCGTCTGCGGCACCGTCCAATC-ATGTGGAT-  
GCCGGAATGGGGATGTCCGG-ACGGCGAATCCGTA-  
TTGCTTGTCCCGTGAGGCCCAGGTGGATGGGGGGAAGGATC-TGGTGTCCGGGATGAT-  
ATGGGGCCGATGCCCGCGTTGAAGTCCACTGGATCGGGAATTCGGGAATCGTGAT-CCGACGTTTCAGGCCGAAC  
(SEQ ID NO. 719)

## Clone X0019

.....X0019SP6.seq:.....  
CTAACGGAATGAAAGCCCTGGTGGCCGT-  
TCGGCGGTGGCCGTCGTCGCACTGCTCGGTGTATCTTCCGCCCAAGCTGATCCCGAGGCGGATCCCGGCCGAGGTGA  
GGCCAATATGGTGGCCCCCAAGTTCCCCACGTCTTGTGATCACACCGAATGGGCGCA-  
TGGGGAATTCTGCCAGCCTCCGGGTCTACCGTCCCAAGTTGGGCGTACA-  
CCTCCCGCCGCTCGGGATGGCCGCTGCCGACCCGGCCTGGGCC-  
AGGTTCTCGCGCTGTCACCGGAAGCCGACACTGCCGGC (SEQ ID NO. 720)

.....X0019T7.seq:.....

CCGCGGACAC-CCTC-  
ATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCCGCCGCGGG  
CGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCGGAGCGACGGCCAAGGC  
GGCGTGCCAGGTGCCCCGGCGCACGGTGCGGACAAGTGGTGTGCGGGTCCCGATCGGCCCA-  
ACGACATCGTGGCGAAGATTGCGCGGGTACCGCGATGATGTGGTGTGTTGGCGACGCCGGCGTTGT

(SEQ ID NO. 721)

## Clone X0020

.....X0020T7.seq:.....

CTCTGGGACCGGCCACGGTGCC-  
CCGGCGTTCCCGGACGTGCTGCGCCAGGTGTCCGGCGGCCGCTGCATGGTGTTCGCGATCGGCCGCTGGCCAGAG  
CCCACCGGTGAATCTGGCGCCTGGCCGACCACCGTGCGCCGTAGGCTTGCGATCGTGCAGCGCTGGCGTGGCCAGGA  
CGAGATCCCGACGGATTGGGGCAGATGCGTGCTCACCATCGGGGTATTTGACGGCGTGCACCGCGGGCACGCCGAAC  
TGATCGCGCACGCGGTCAAAGGCGGC (SEQ ID NO. 722)

## Clone X0021

.....X0021SP6.seq:.....

AATACTCAAGCTTTCGTCACTTCATTGCGCCAGCAGACCAACAA-AGCATCGGGACATACGGA-  
TCAACTACCCGGCCAAACGGTGATTTCTTGCCGCGCGTGACGGCGCGAACGACGCCAGCGACCAC-  
TTCAGCAAATGGCCA-CGCGTGCCGGGCCACGAGTTGGTGTGCTCGGCGGCTACTCCAGGGTGCGGCCGTGATC-  
ACATC-TCACCGCCGCACCACTGCCCGGCCTCGGGTTACGCGAGCCGTTGCCGCCCGCAGCGGAC-  
ATCACATCGCCGCGATCGCCCTGTTCCGGAATCCCTC-GGCCGCGCTGGCGGGCTGATTAAC (SEQ ID NO. 723)

.....X0021T7.seq:.....

TGCCGCGGATTTGGCTGGCTGCCAATATTAGAATCGGGCCTTTCTTTTGGCGGACAATAAGGTCACAGTAAACC  
CTCGTTTTGTGAGATGCGGGGCGGGCCGGGCGAA-  
TCGACCTCGAGTGAATGGATCTCGAGTGAATGGACAGGGCATCGCCTACGAGTCGCATCCCCATCCAACAGACCGGT  
GCTCTTGATCGGACCCTGAAGGTCCCGCACGGAGGGTGTGTTGCCGGCGCGGGGTACGGTGCGGTAGCGACGTA  
GTGTTTGAACGAATTTCTTGATGCTCCAACCTGTTTGGTGTTCATCCAGTTCT (SEQ ID NO. 724)

## Clone X0175

.....X0175SP6.....

AA-CTTGCGCGCTCGGCCGGGTC-AGCATCCAGCTGCTCGGCAAGGAGGCCAGCTAC-C-  
TCGCTGCGTATGCCAGCGGTGAGATCCGCCGGGTC-  
ACGTCCGCTGCCGCGGACCGTCGGCGAAGTGGGCAATGCCGAGCAGGCAAACATCAACTGGGGCAAGGCCGGTCCG  
ATGCGGTGGAAGGGCAAGCGCCCGTCGGTCCGGGGCGTGTTGAT-AACCCGGTC-  
ACCACCGCACGCGGTGGTGAGGGTAAACCTCCGGCGGCCGTCACCCGGTTAGCCCGTGGGGCAA

(SEQ ID NO. 725)

.....X0175T7.....

A-TCGAAAGTGACCATCTCTACCTTGAGTGCCATACCGCCCGACCTATGCCTCGGATAGCTCGGCGGAAAGAAACG  
CTTGCACTGCCGCCGAATAGGCGGCTACGTCTGAGCGCCCATCAACTCTCGCGCGGAGTGCATCGCCAGCTGGGCG  
GCGCCGACGTGACCGTGGGGATTCCGGTGCGCGCCGCGGCCAACGGCCCGATCGTCGACCCGCACGGCAGATCGGC  
GCGATGTTCTGAACGCTGCATAGGCACTCCCGCGCGCTGGCAGGCCAGTGCGAACGCCGCCGCGGTGCGTCCG

(SEQ ID NO. 726)

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